



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 13, 2024 – 11:10 pm GMT

PDB ID : 6REZ  
Title : Crystal structure of the light-driven sodium pump KR2 in the pentameric form, pH 5.0  
Authors : Kovalev, K.; Polovinkin, V.; Gushchin, I.; Borshchevskiy, V.; Gordeliy, V.  
Deposited on : 2019-04-12  
Resolution : 2.60 Å(reported)

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A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.8.4, CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.36  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36

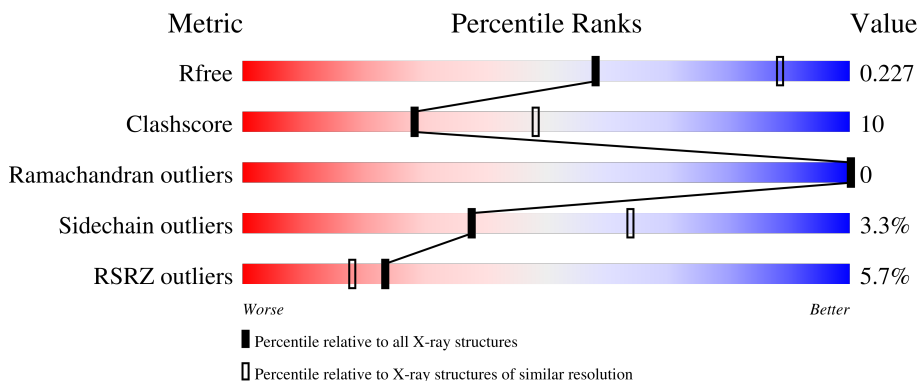
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	273	 7% 86% 13%
1	B	273	 6% 85% 13%
1	C	273	 5% 86% 13%
1	D	273	 5% 86% 12%
1	E	273	 5% 89% 10%

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

<b>Mol</b>	<b>Type</b>	<b>Chain</b>	<b>Res</b>	<b>Chirality</b>	<b>Geometry</b>	<b>Clashes</b>	<b>Electron density</b>
2	LFA	C	307	-	-	-	X

## 2 Entry composition [i](#)

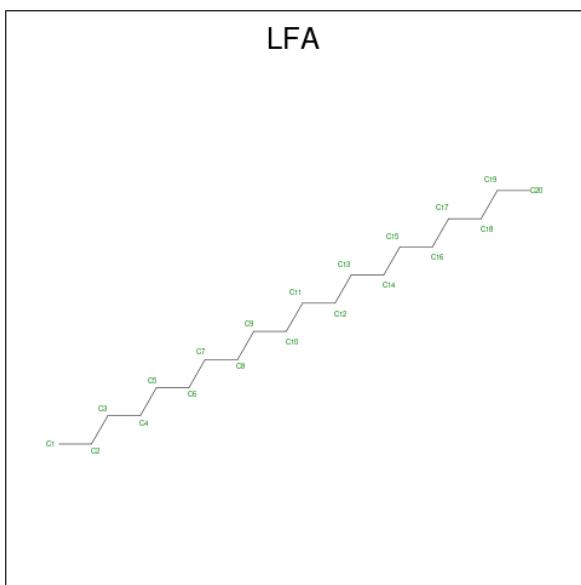
There are 6 unique types of molecules in this entry. The entry contains 11529 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Sodium pumping rhodopsin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	273	Total 2193	C 1460	N 332	O 392	S 9	0	3	0
1	B	273	Total 2185	C 1454	N 332	O 390	S 9	0	3	0
1	C	273	Total 2190	C 1458	N 331	O 392	S 9	0	3	0
1	D	270	Total 2162	C 1440	N 327	O 386	S 9	0	3	0
1	E	273	Total 2180	C 1452	N 330	O 389	S 9	0	3	0

- Molecule 2 is EICOSANE (three-letter code: LFA) (formula: C<sub>20</sub>H<sub>42</sub>).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total 18	C 18	0	0

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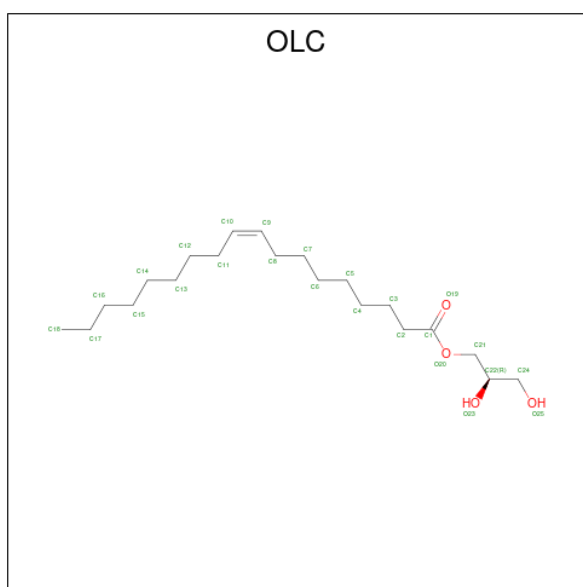
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total C 16 16	0	0
2	A	1	Total C 5 5	0	0
2	A	1	Total C 11 11	0	0
2	A	1	Total C 15 15	0	0
2	A	1	Total C 7 7	0	0
2	B	1	Total C 17 17	0	0
2	B	1	Total C 18 18	0	0
2	B	1	Total C 5 5	0	0
2	B	1	Total C 10 10	0	0
2	B	1	Total C 6 6	0	0
2	B	1	Total C 16 16	0	0
2	C	1	Total C 19 19	0	0
2	C	1	Total C 10 10	0	0
2	C	1	Total C 5 5	0	0
2	C	1	Total C 16 16	0	0
2	C	1	Total C 10 10	0	0
2	C	1	Total C 17 17	0	0
2	C	1	Total C 7 7	0	0
2	D	1	Total C 17 17	0	0
2	D	1	Total C 5 5	0	0
2	D	1	Total C 16 16	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	D	1	Total C 6 6	0	0
2	D	1	Total C 16 16	0	0
2	E	1	Total C 15 15	0	0
2	E	1	Total C 16 16	0	0
2	E	1	Total C 5 5	0	0
2	E	1	Total C 10 10	0	0
2	E	1	Total C 15 15	0	0
2	E	1	Total C 9 9	0	0
2	E	1	Total C 9 9	0	0

- Molecule 3 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: C<sub>21</sub>H<sub>40</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total C O 10 6 4	0	0
3	B	1	Total C O 10 6 4	0	0

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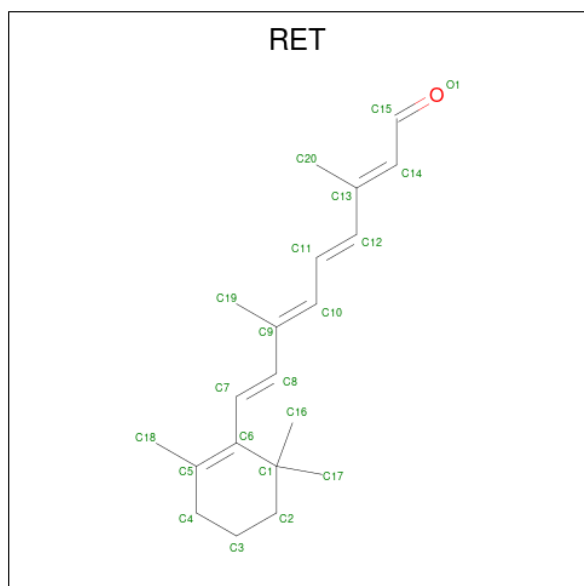
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total C O 11 7 4	0	0
3	D	1	Total C O 9 5 4	0	0
3	E	1	Total C O 10 7 3	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total Na 1 1	0	0
4	B	1	Total Na 1 1	0	0
4	C	1	Total Na 1 1	0	0
4	D	1	Total Na 1 1	0	0
4	E	1	Total Na 1 1	0	0

- Molecule 5 is RETINAL (three-letter code: RET) (formula: C<sub>20</sub>H<sub>28</sub>O).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C 20 20	0	0

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	B	1	Total C 20 20	0	0
5	C	1	Total C 20 20	0	0
5	D	1	Total C 20 20	0	0
5	E	1	Total C 20 20	0	0

- Molecule 6 is water.

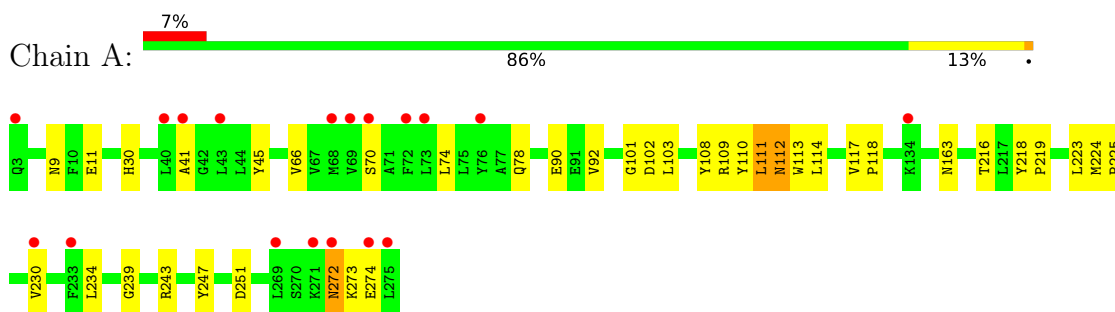
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	17	Total O 17 17	0	0
6	B	19	Total O 19 19	0	0
6	C	22	Total O 22 22	0	0
6	D	18	Total O 18 18	0	0
6	E	21	Total O 21 21	0	0



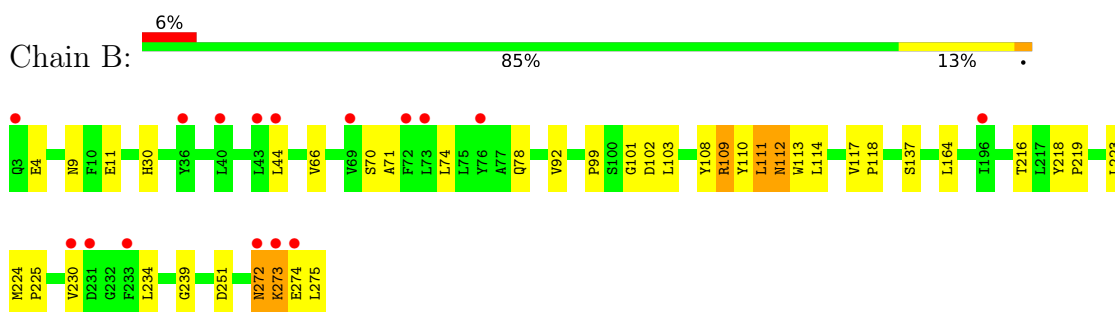
### 3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ( $RSRZ > 2$ ). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

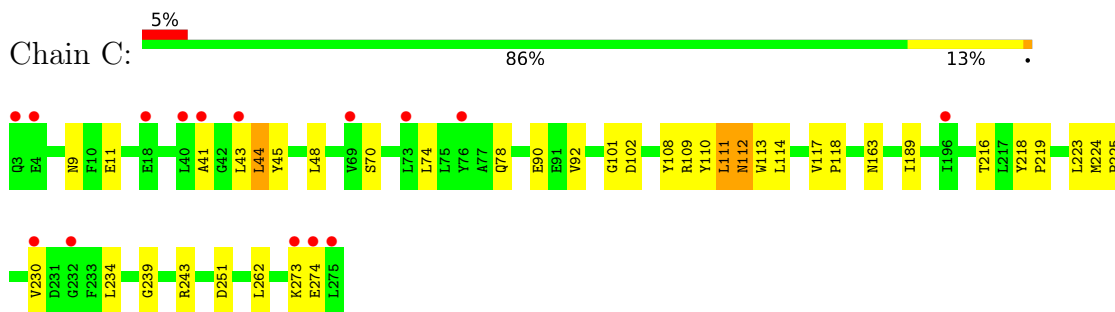
- Molecule 1: Sodium pumping rhodopsin



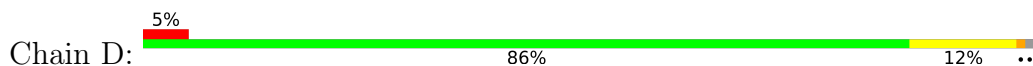
- Molecule 1: Sodium pumping rhodopsin

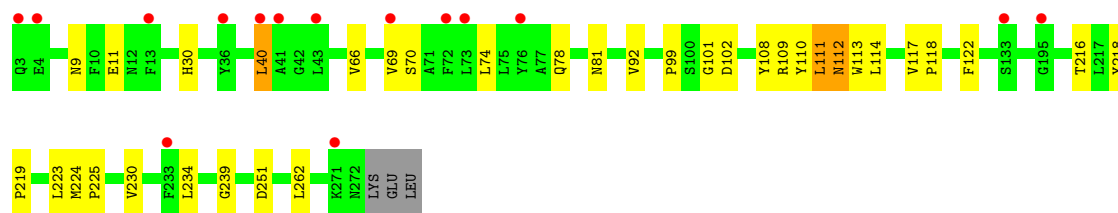


- Molecule 1: Sodium pumping rhodopsin

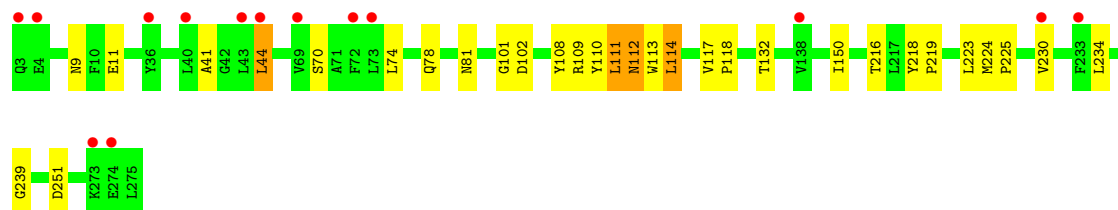
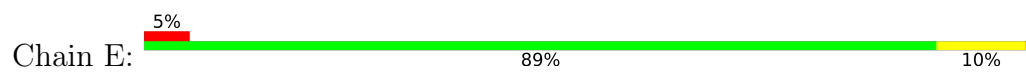


- Molecule 1: Sodium pumping rhodopsin





● Molecule 1: Sodium pumping rhodopsin



## 4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	130.24Å 241.39Å 135.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.13 – 2.60 48.08 – 2.60	Depositor EDS
% Data completeness (in resolution range)	98.6 (48.13-2.60) 98.7 (48.08-2.60)	Depositor EDS
$R_{merge}$	0.09	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.39 (at 2.61Å)	Xtrriage
Refinement program	REFMAC 5.8.0230	Depositor
R, $R_{free}$	0.191 , 0.225 0.200 , 0.227	Depositor DCC
$R_{free}$ test set	3301 reflections (5.10%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	71.4	Xtrriage
Anisotropy	0.408	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.33 , 60.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.52$ , $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	11529	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	76.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: LFA, RET, OLC, NA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 5$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# Z  >5	RMSZ	# Z  >5
1	A	0.27	0/2251	0.41	0/3061
1	B	0.27	0/2243	0.40	0/3052
1	C	0.27	0/2248	0.41	0/3058
1	D	0.27	0/2218	0.40	0/3014
1	E	0.27	0/2238	0.41	0/3046
All	All	0.27	0/11198	0.41	0/15231

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

### 5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2193	0	2162	48	0
1	B	2185	0	2150	48	0
1	C	2190	0	2153	47	0
1	D	2162	0	2118	40	0
1	E	2180	0	2140	31	0
2	A	72	0	135	2	0
2	B	72	0	138	2	0
2	C	84	0	161	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	60	0	115	0	0
2	E	79	0	151	0	0
3	A	10	0	9	4	0
3	B	10	0	9	0	0
3	C	11	0	11	4	0
3	D	9	0	7	0	0
3	E	10	0	8	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
5	A	20	0	27	5	0
5	B	20	0	27	7	0
5	C	20	0	27	5	0
5	D	20	0	27	7	0
5	E	20	0	27	6	0
6	A	17	0	0	3	0
6	B	19	0	0	5	0
6	C	22	0	0	2	0
6	D	18	0	0	3	0
6	E	21	0	0	2	0
All	All	11529	0	11602	227	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 10.

The worst 5 of 227 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:112[B]:ASN:ND2	6:B:402:HOH:O	1.69	1.25
1:C:74[B]:LEU:HD23	1:C:112[B]:ASN:OD1	1.32	1.23
1:B:112[B]:ASN:OD1	6:B:401:HOH:O	1.57	1.20
1:C:74[B]:LEU:HD23	1:C:112[B]:ASN:CG	1.65	1.16
1:A:112[B]:ASN:ND2	6:A:402:HOH:O	1.84	1.06

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	274/273 (100%)	266 (97%)	8 (3%)	0	100	100
1	B	274/273 (100%)	266 (97%)	8 (3%)	0	100	100
1	C	274/273 (100%)	266 (97%)	8 (3%)	0	100	100
1	D	270/273 (99%)	262 (97%)	8 (3%)	0	100	100
1	E	274/273 (100%)	266 (97%)	8 (3%)	0	100	100
All	All	1366/1365 (100%)	1326 (97%)	40 (3%)	0	100	100

There are no Ramachandran outliers to report.

### 5.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	232/234 (99%)	224 (97%)	8 (3%)	37	63
1	B	231/234 (99%)	219 (95%)	12 (5%)	23	46
1	C	231/234 (99%)	222 (96%)	9 (4%)	32	58
1	D	227/234 (97%)	221 (97%)	6 (3%)	46	72
1	E	229/234 (98%)	222 (97%)	7 (3%)	40	66
All	All	1150/1170 (98%)	1108 (96%)	42 (4%)	38	60

5 of 42 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	274	GLU
1	E	44	LEU
1	D	40	LEU
1	D	112[A]	ASN
1	E	112[A]	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 9 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	3	GLN
1	E	180	HIS
1	B	272	ASN
1	C	163	ASN
1	C	180	HIS

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

## 5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 46 ligands modelled in this entry, 5 are monoatomic - leaving 41 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	LFA	D	306	-	15,15,19	0.33	0	14,14,18	0.43	0
3	OLC	D	302	-	8,8,24	1.03	1 (12%)	9,9,25	1.05	1 (11%)
5	RET	C	310	1	20,20,21	0.75	0	27,27,28	1.64	5 (18%)
2	LFA	E	301	-	14,14,19	0.35	0	13,13,18	0.39	0
2	LFA	A	306	-	14,14,19	0.31	0	13,13,18	0.44	0
2	LFA	A	302	-	15,15,19	0.33	0	14,14,18	0.41	0
3	OLC	C	302	-	10,10,24	1.43	1 (10%)	11,11,25	1.28	2 (18%)
2	LFA	C	308	-	6,6,19	0.33	0	5,5,18	0.29	0
2	LFA	C	306	-	9,9,19	0.28	0	8,8,18	0.44	0
2	LFA	A	307	-	6,6,19	0.32	0	5,5,18	0.28	0
5	RET	B	309	1	20,20,21	0.77	0	27,27,28	1.68	5 (18%)
2	LFA	E	304	-	4,4,19	0.28	0	3,3,18	0.35	0
2	LFA	B	306	-	5,5,19	0.28	0	4,4,18	0.36	0
2	LFA	E	306	-	14,14,19	0.32	0	13,13,18	0.44	0
2	LFA	A	301	-	17,17,19	0.31	0	16,16,18	0.48	0
2	LFA	E	302	-	15,15,19	0.30	0	14,14,18	0.48	0
2	LFA	C	301	-	18,18,19	0.31	0	17,17,18	0.47	0
2	LFA	B	302	-	17,17,19	0.31	0	16,16,18	0.45	0
2	LFA	D	305	-	5,5,19	0.31	0	4,4,18	0.28	0
2	LFA	E	307	-	8,8,19	0.30	0	7,7,18	0.41	0
2	LFA	D	304	-	15,15,19	0.30	0	14,14,18	0.46	0
2	LFA	A	304	-	4,4,19	0.28	0	3,3,18	0.36	0
2	LFA	C	305	-	15,15,19	0.33	0	14,14,18	0.43	0
2	LFA	B	307	-	15,15,19	0.33	0	14,14,18	0.45	0
2	LFA	D	303	-	4,4,19	0.30	0	3,3,18	0.33	0
3	OLC	E	303	-	9,9,24	1.50	1 (11%)	9,9,25	1.27	2 (22%)
2	LFA	C	304	-	4,4,19	0.29	0	3,3,18	0.35	0
2	LFA	C	303	-	9,9,19	0.29	0	8,8,18	0.45	0
2	LFA	B	301	-	16,16,19	0.29	0	15,15,18	0.46	0
2	LFA	B	304	-	4,4,19	0.29	0	3,3,18	0.33	0
3	OLC	B	303	-	9,9,24	1.53	1 (11%)	10,10,25	1.44	2 (20%)
2	LFA	B	305	-	9,9,19	0.30	0	8,8,18	0.42	0
2	LFA	D	301	-	16,16,19	0.30	0	15,15,18	0.48	0
2	LFA	E	308	-	8,8,19	0.30	0	7,7,18	0.40	0
5	RET	E	310	1	20,20,21	0.75	0	27,27,28	1.65	5 (18%)
5	RET	D	308	1	20,20,21	0.72	0	27,27,28	1.63	4 (14%)
5	RET	A	309	1	20,20,21	0.66	0	27,27,28	1.69	7 (25%)
2	LFA	C	307	-	16,16,19	0.30	0	15,15,18	0.47	0
2	LFA	A	305	-	10,10,19	0.32	0	9,9,18	0.44	0
3	OLC	A	303	-	9,9,24	1.48	1 (11%)	10,10,25	1.46	2 (20%)
2	LFA	E	305	-	9,9,19	0.30	0	8,8,18	0.42	0



In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	LFA	D	306	-	-	7/13/13/17	-
3	OLC	D	302	-	-	6/7/7/24	-
5	RET	C	310	1	-	0/13/30/31	0/1/1/1
2	LFA	E	301	-	-	4/12/12/17	-
2	LFA	A	306	-	-	7/12/12/17	-
2	LFA	A	302	-	-	7/13/13/17	-
3	OLC	C	302	-	-	5/10/10/24	-
2	LFA	C	308	-	-	1/4/4/17	-
2	LFA	C	306	-	-	2/7/7/17	-
2	LFA	A	307	-	-	2/4/4/17	-
5	RET	B	309	1	-	0/13/30/31	0/1/1/1
2	LFA	E	304	-	-	1/2/2/17	-
2	LFA	B	306	-	-	1/3/3/17	-
2	LFA	E	306	-	-	7/12/12/17	-
2	LFA	A	301	-	-	5/15/15/17	-
2	LFA	E	302	-	-	5/13/13/17	-
2	LFA	C	301	-	-	13/16/16/17	-
2	LFA	B	302	-	-	8/15/15/17	-
2	LFA	D	305	-	-	1/3/3/17	-
2	LFA	E	307	-	-	4/6/6/17	-
2	LFA	D	304	-	-	6/13/13/17	-
2	LFA	A	304	-	-	1/2/2/17	-
2	LFA	C	305	-	-	11/13/13/17	-
2	LFA	B	307	-	-	5/13/13/17	-
2	LFA	D	303	-	-	1/2/2/17	-
3	OLC	E	303	-	-	3/8/8/24	-
2	LFA	C	304	-	-	1/2/2/17	-
2	LFA	C	303	-	-	4/7/7/17	-
2	LFA	B	301	-	-	3/14/14/17	-
2	LFA	B	304	-	-	2/2/2/17	-
3	OLC	B	303	-	-	6/9/9/24	-
2	LFA	B	305	-	-	6/7/7/17	-
2	LFA	D	301	-	-	6/14/14/17	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	LFA	E	308	-	-	3/6/6/17	-
5	RET	E	310	1	-	0/13/30/31	0/1/1/1
5	RET	D	308	1	-	0/13/30/31	0/1/1/1
5	RET	A	309	1	-	0/13/30/31	0/1/1/1
2	LFA	C	307	-	-	7/14/14/17	-
2	LFA	A	305	-	-	4/8/8/17	-
3	OLC	A	303	-	-	7/9/9/24	-
2	LFA	E	305	-	-	2/7/7/17	-

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	303	OLC	O20-C1	4.45	1.46	1.33
3	C	302	OLC	O20-C1	4.34	1.46	1.33
3	A	303	OLC	O20-C1	4.29	1.45	1.33
3	E	303	OLC	O20-C1	4.27	1.45	1.33
3	D	302	OLC	O20-C1	2.61	1.46	1.33

The worst 5 of 35 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	B	309	RET	C18-C5-C6	-4.68	119.27	124.53
5	A	309	RET	C18-C5-C6	-4.64	119.32	124.53
5	E	310	RET	C18-C5-C6	-4.54	119.43	124.53
5	D	308	RET	C18-C5-C6	-4.44	119.54	124.53
5	C	310	RET	C18-C5-C6	-4.36	119.64	124.53

There are no chirality outliers.

5 of 164 torsion outliers are listed below:

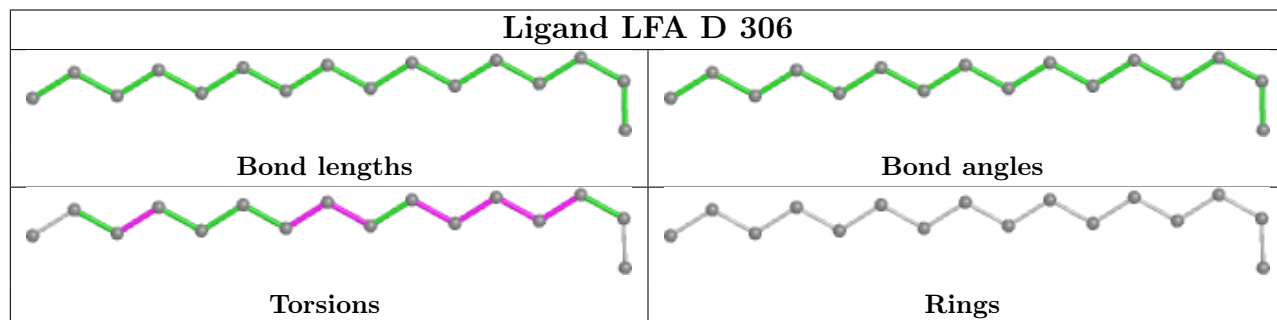
Mol	Chain	Res	Type	Atoms
3	A	303	OLC	O20-C21-C22-C24
3	A	303	OLC	O20-C21-C22-O23
3	B	303	OLC	C21-C22-C24-O25
3	C	302	OLC	O20-C21-C22-O23
3	D	302	OLC	O20-C21-C22-C24

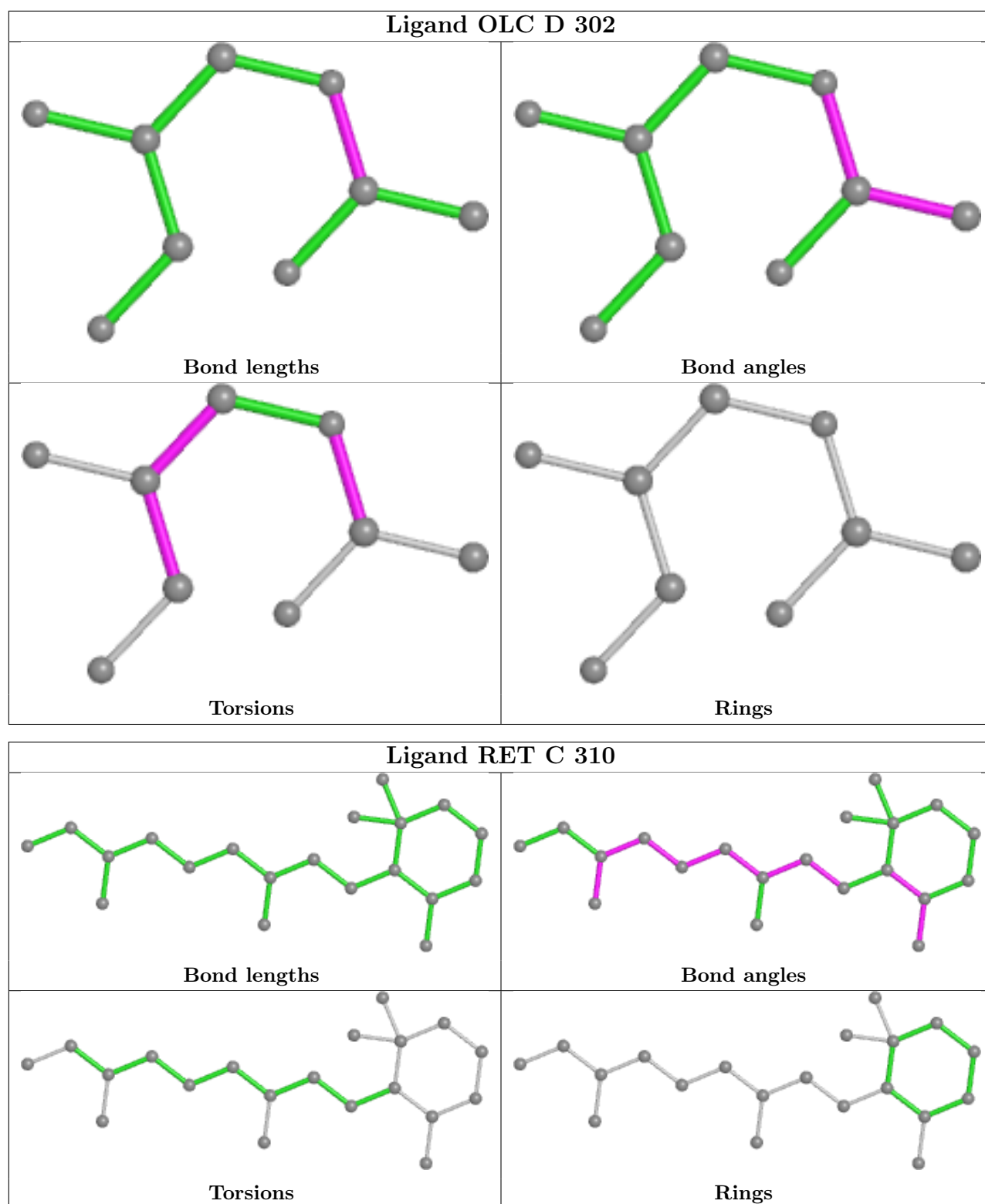
There are no ring outliers.

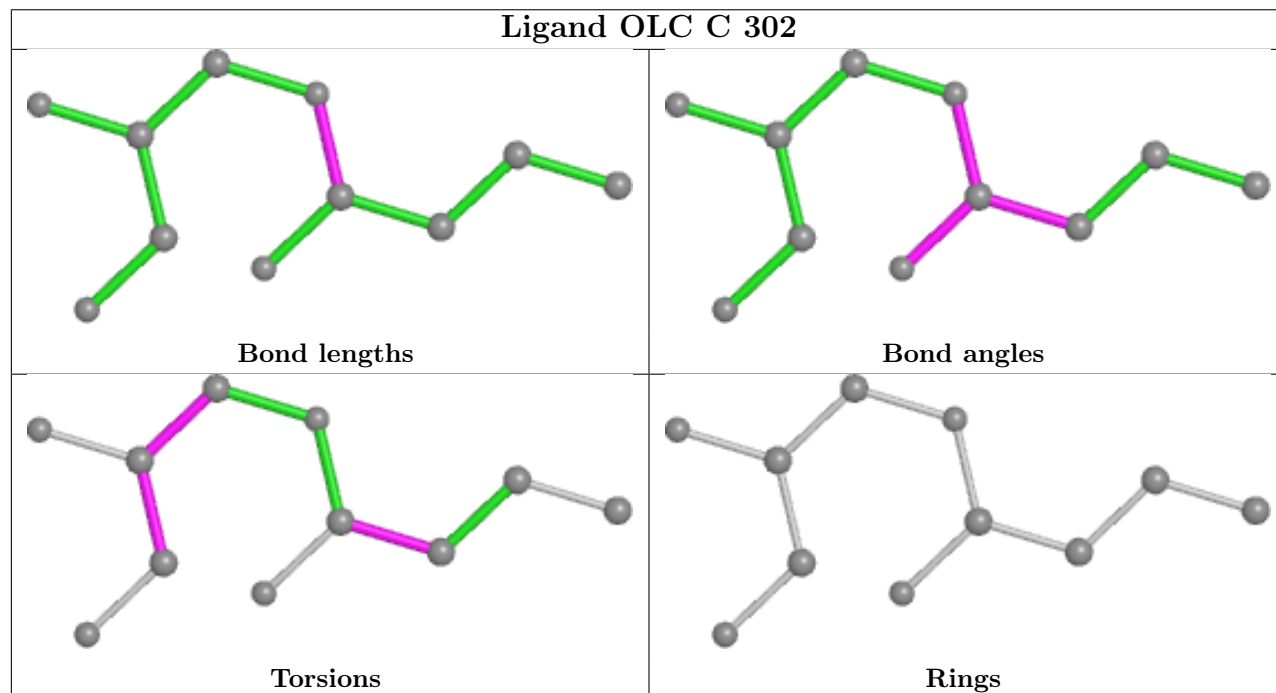
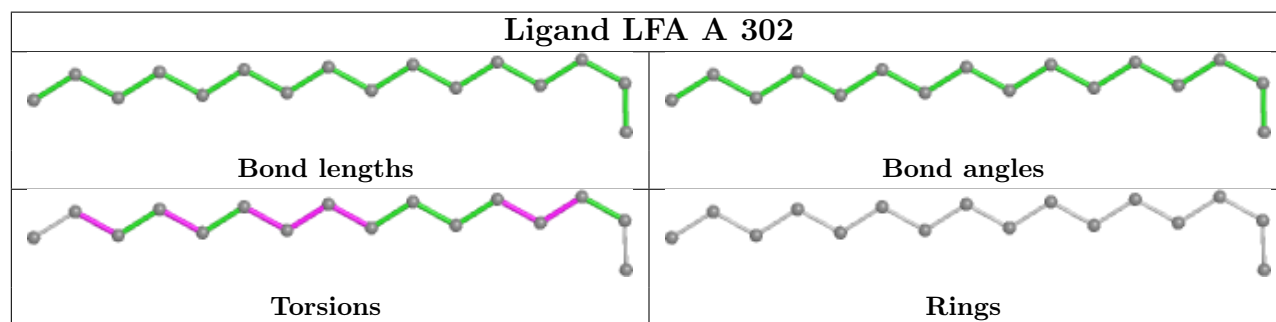
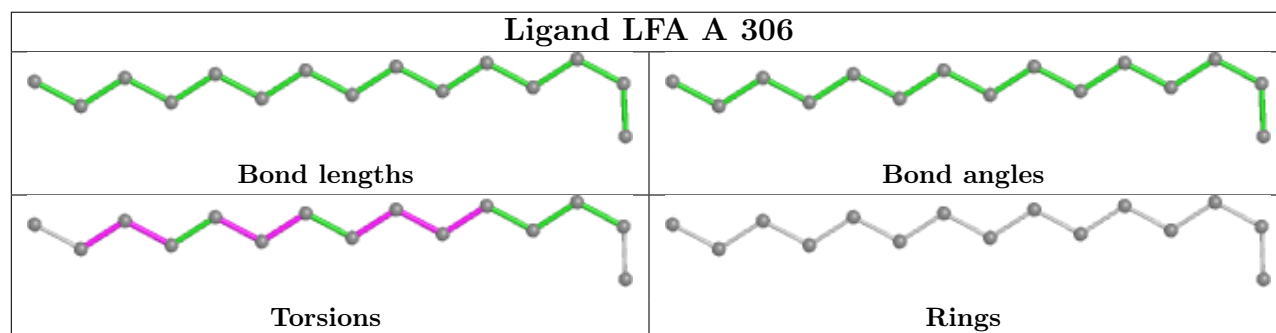
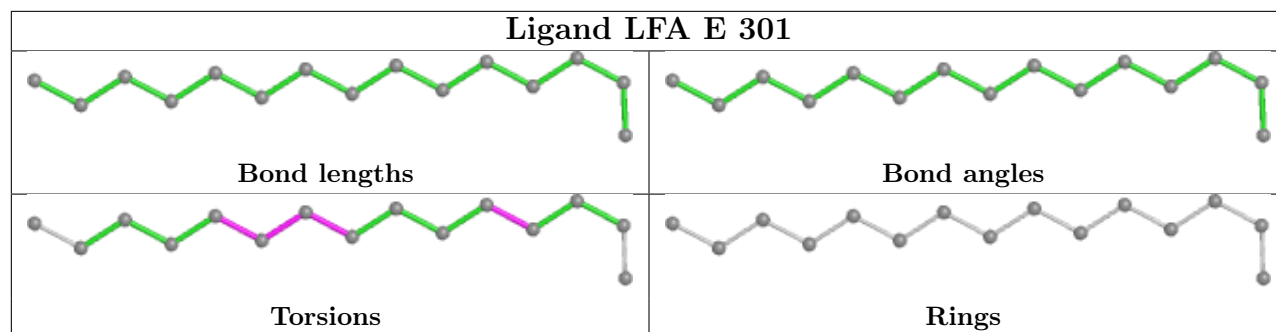
11 monomers are involved in 42 short contacts:

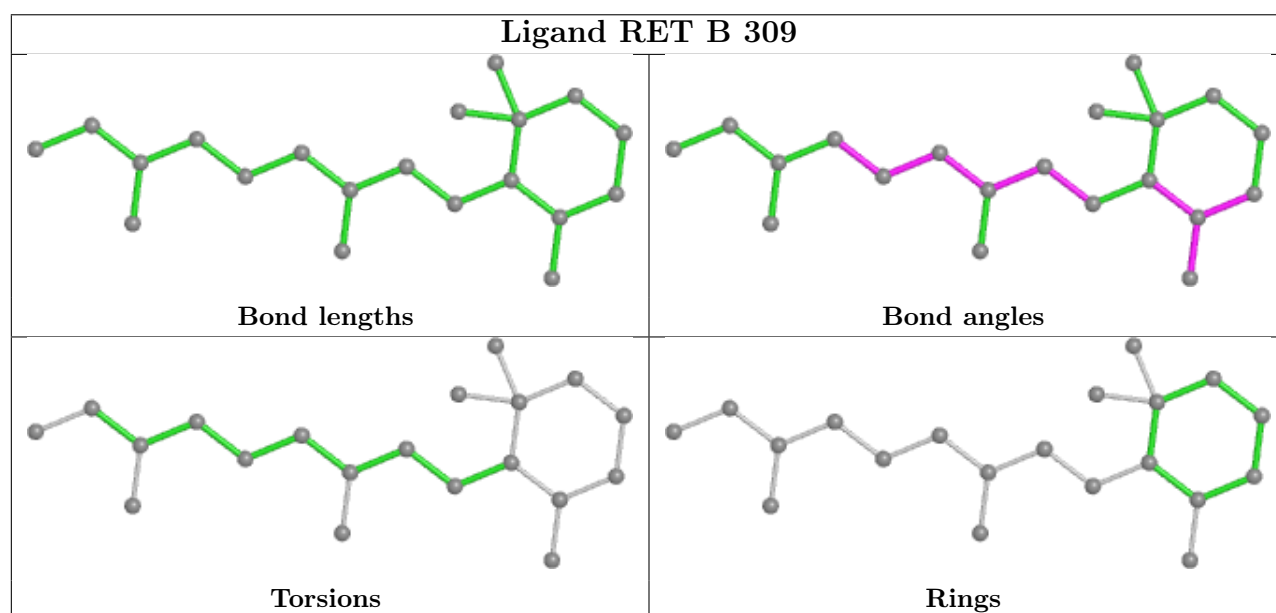
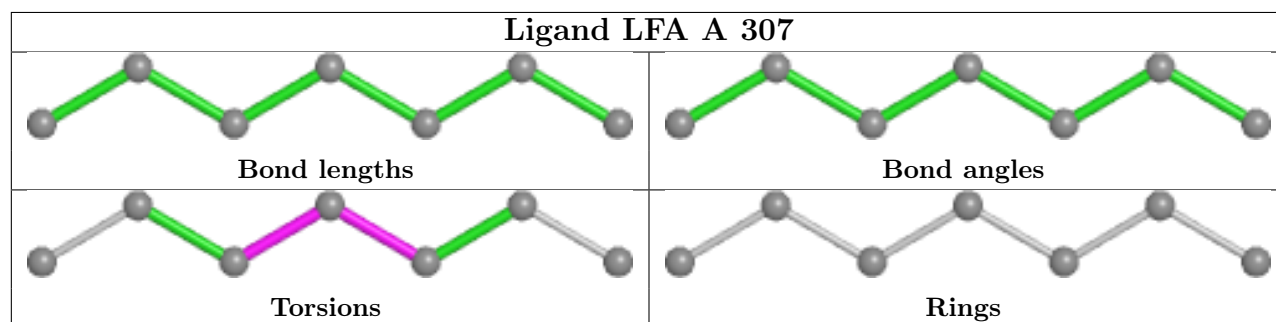
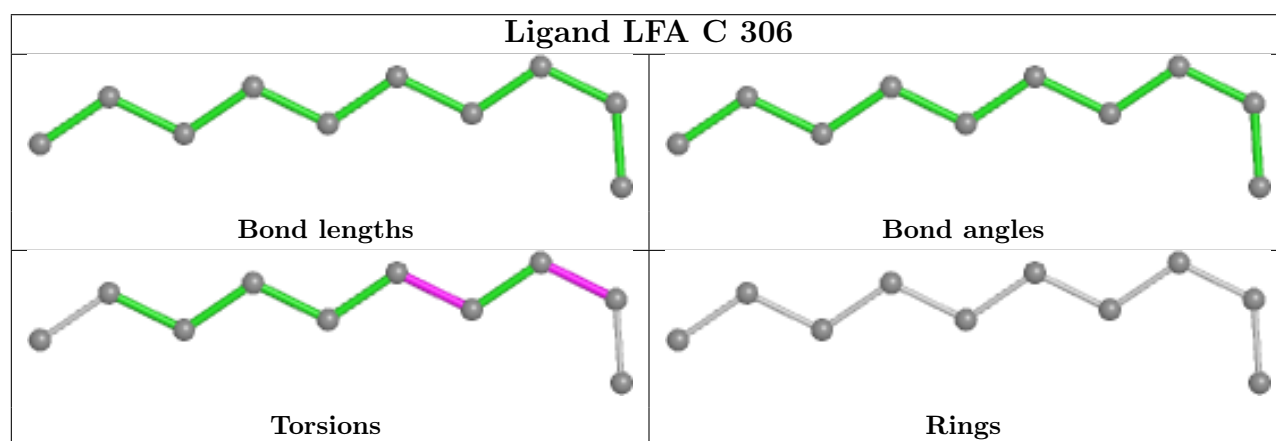
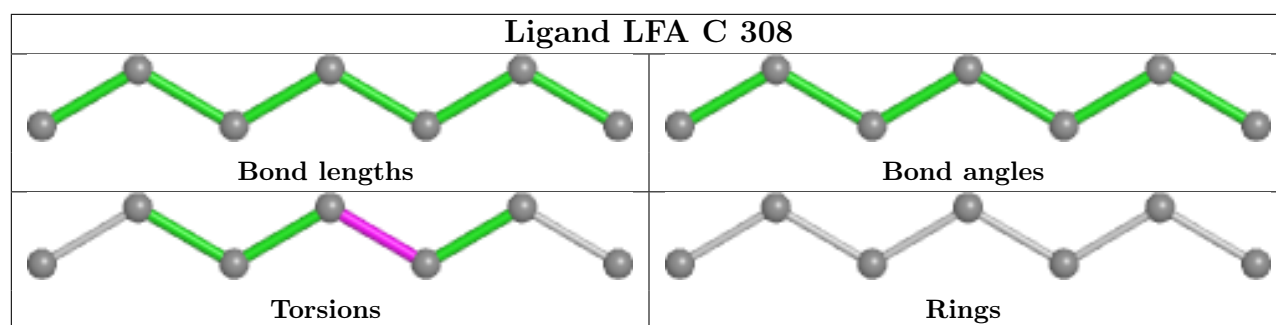
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	C	310	RET	5	0
3	C	302	OLC	4	0
5	B	309	RET	7	0
2	B	306	LFA	1	0
2	A	301	LFA	2	0
2	C	301	LFA	1	0
2	B	302	LFA	2	0
5	E	310	RET	6	0
5	D	308	RET	7	0
5	A	309	RET	5	0
3	A	303	OLC	4	0

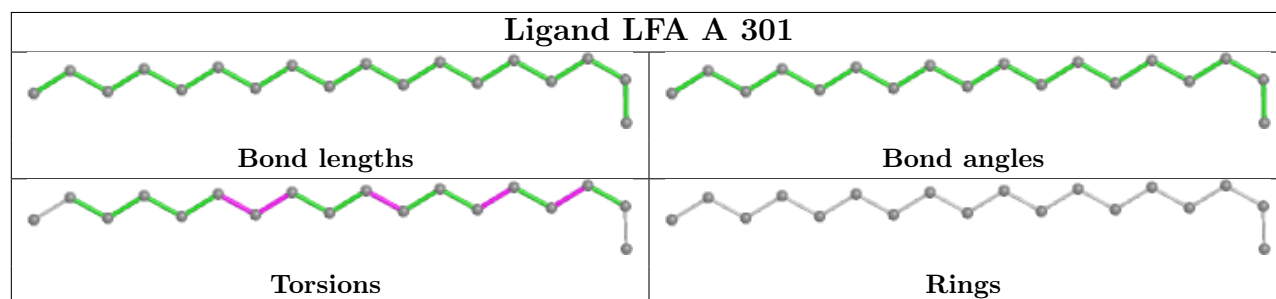
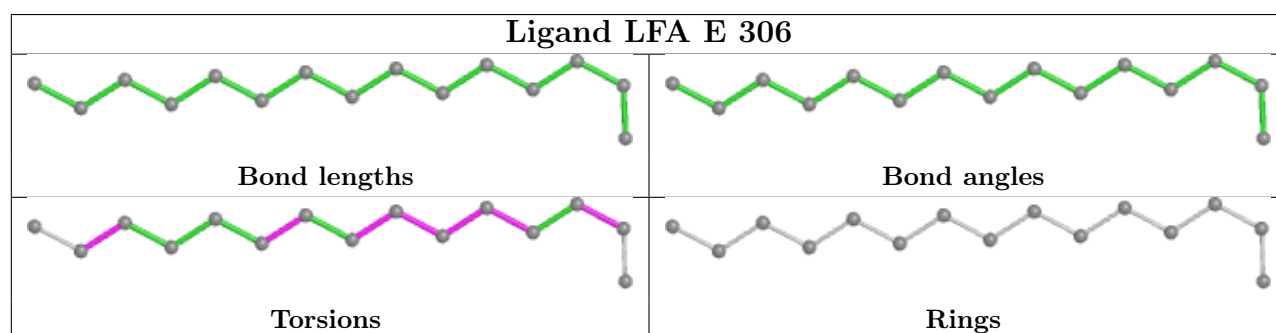
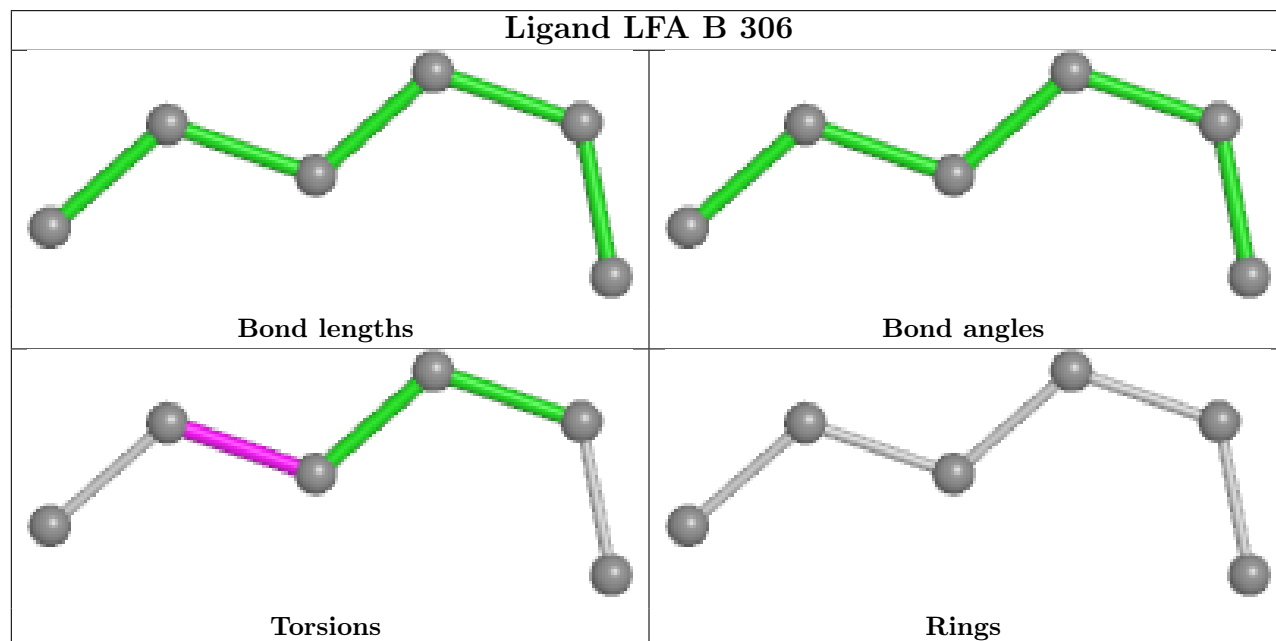
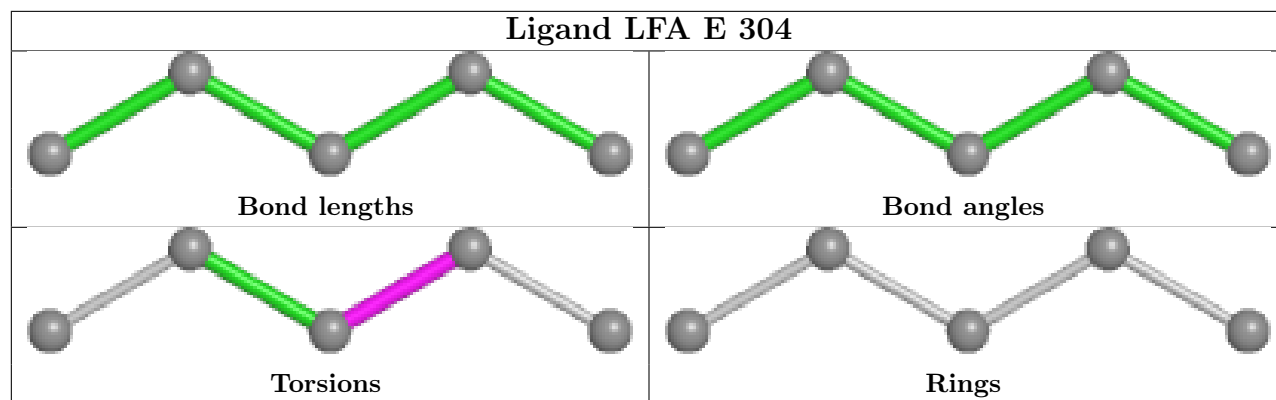
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

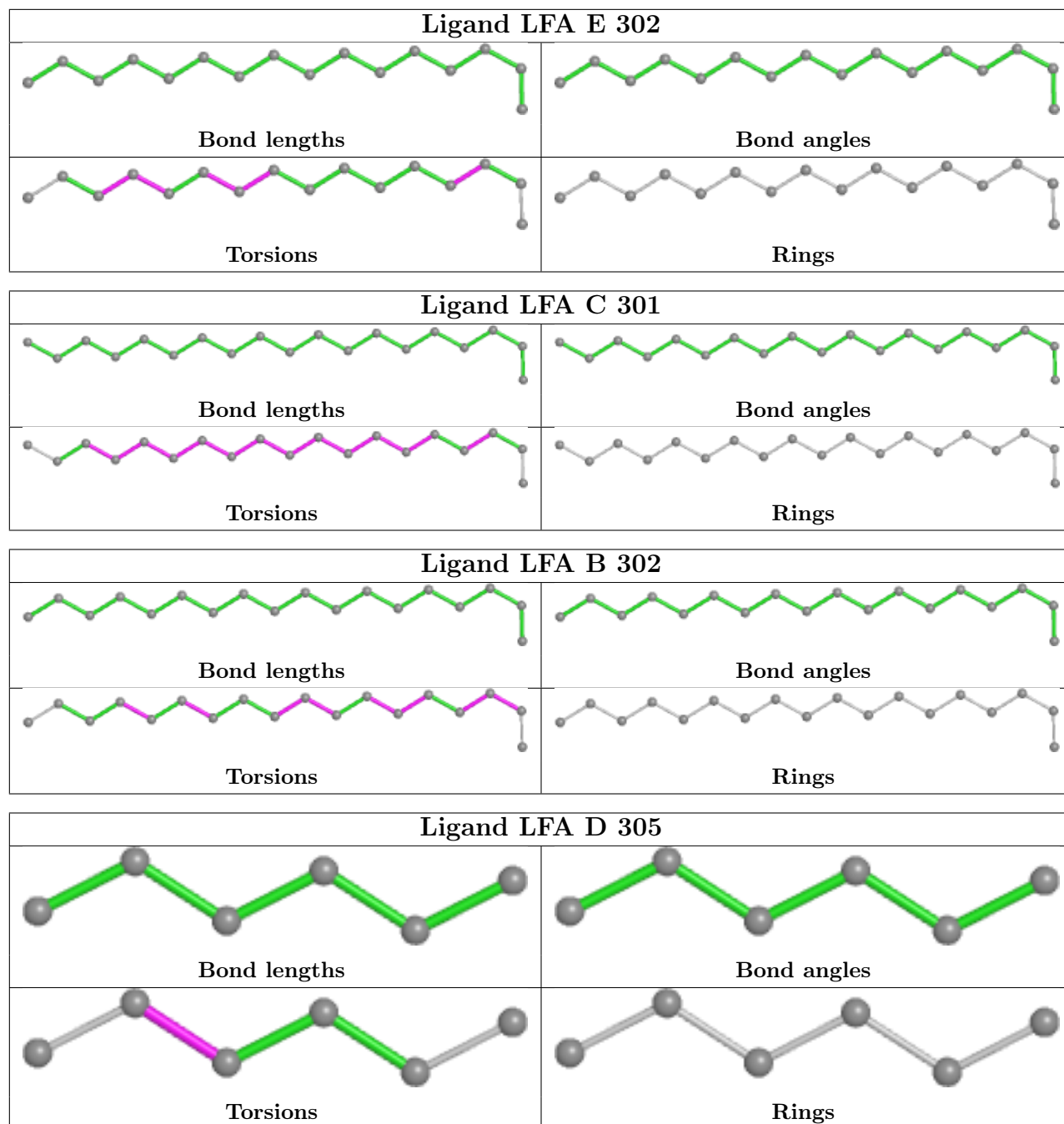




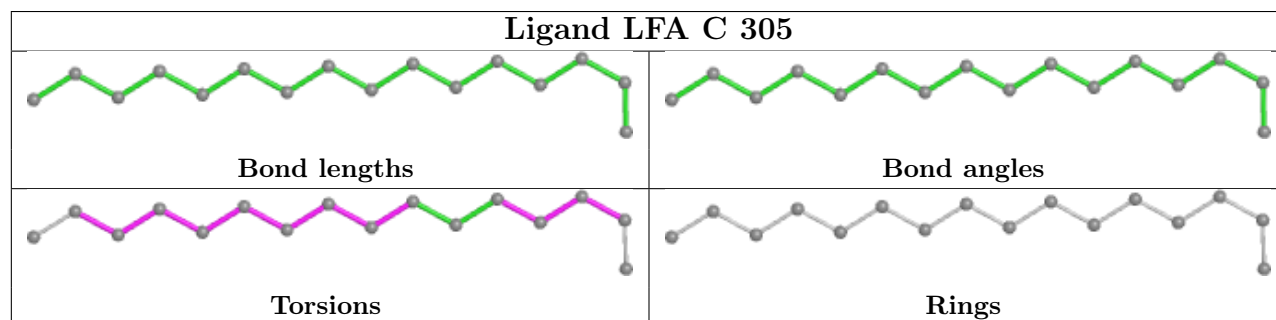
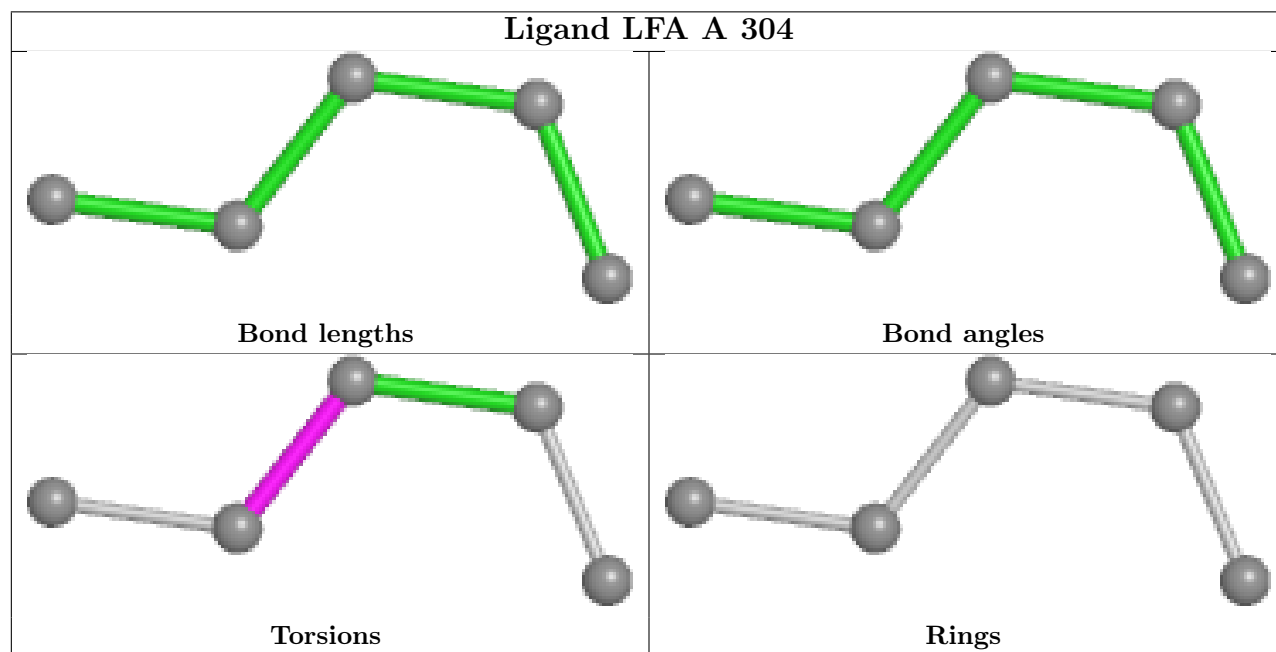
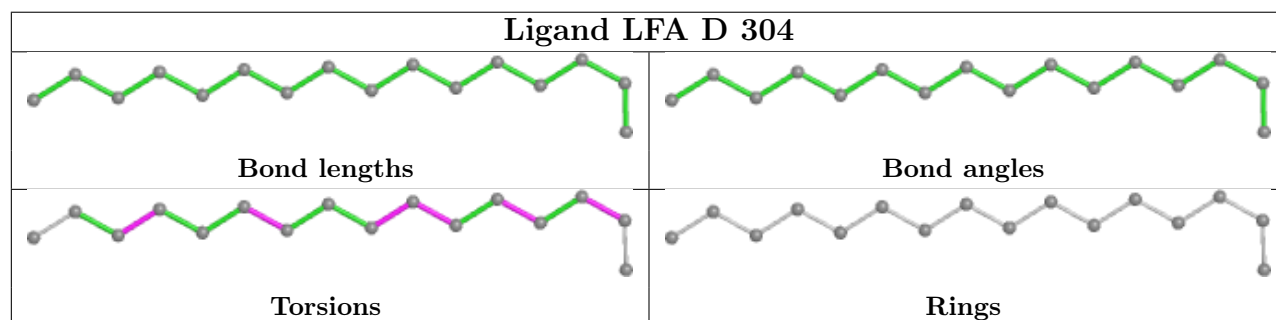
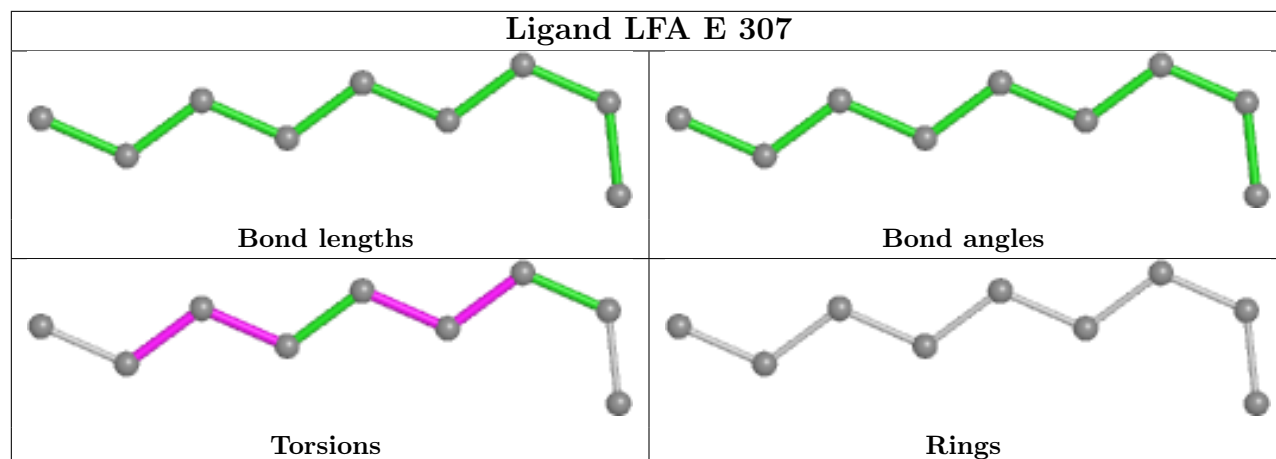


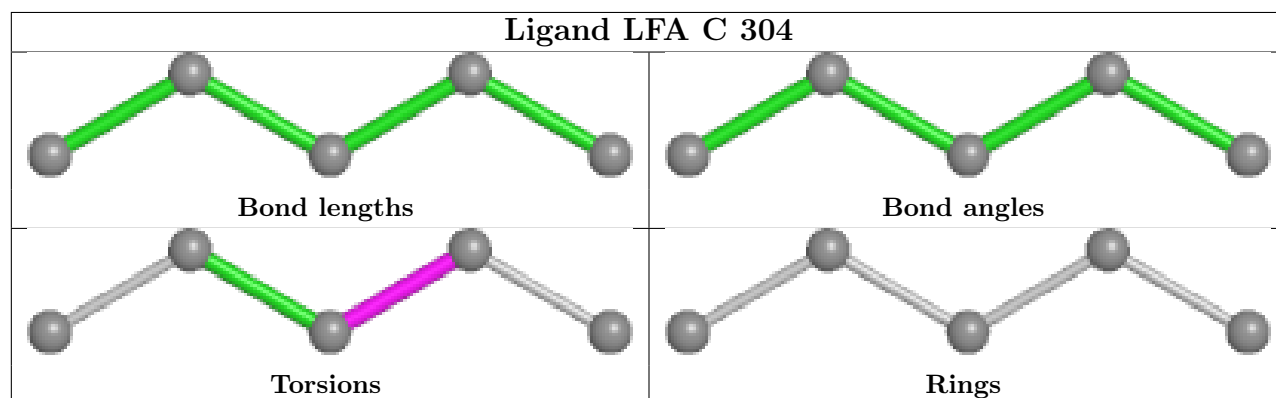
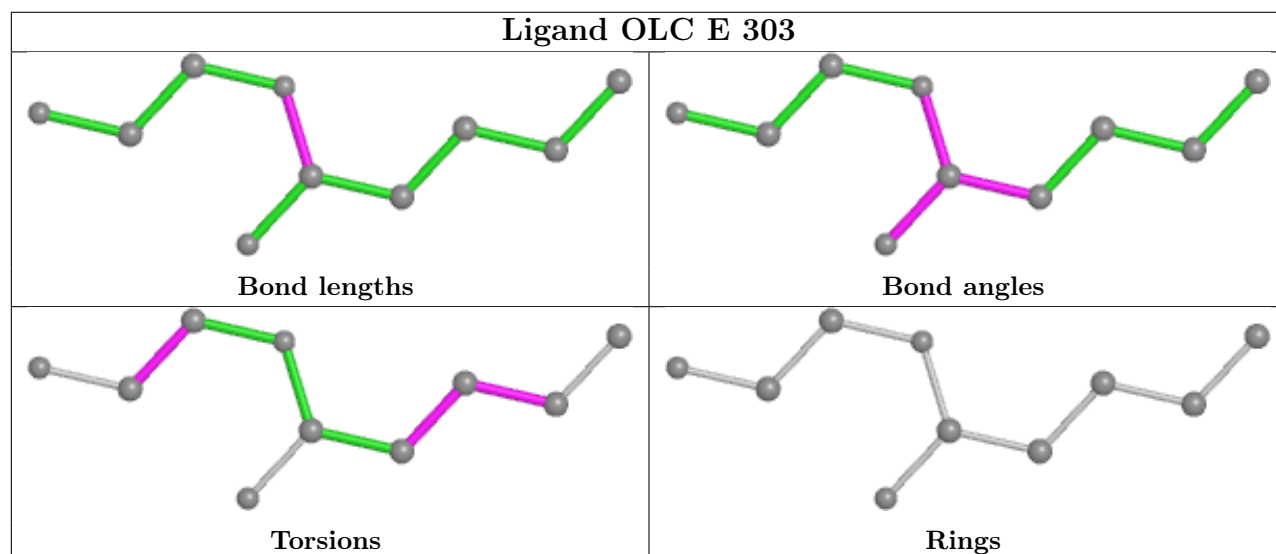
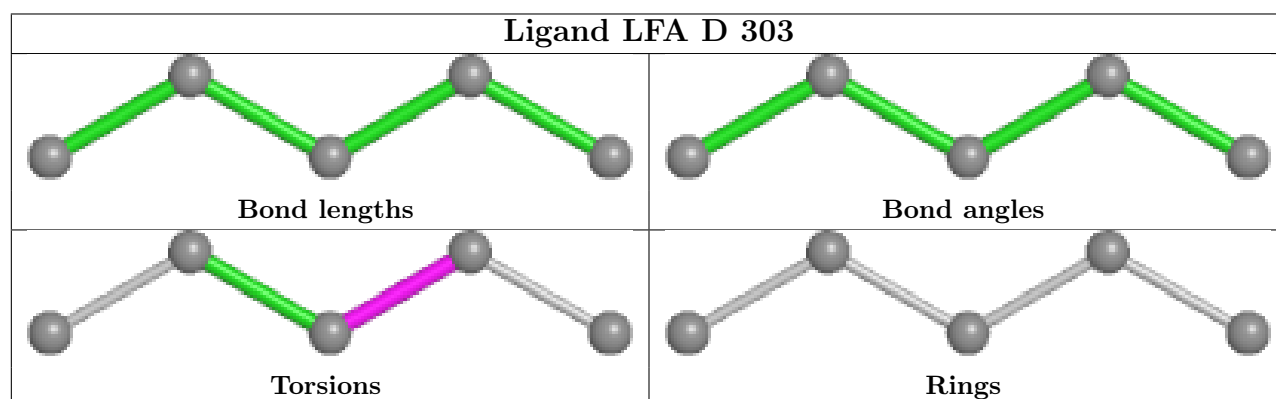
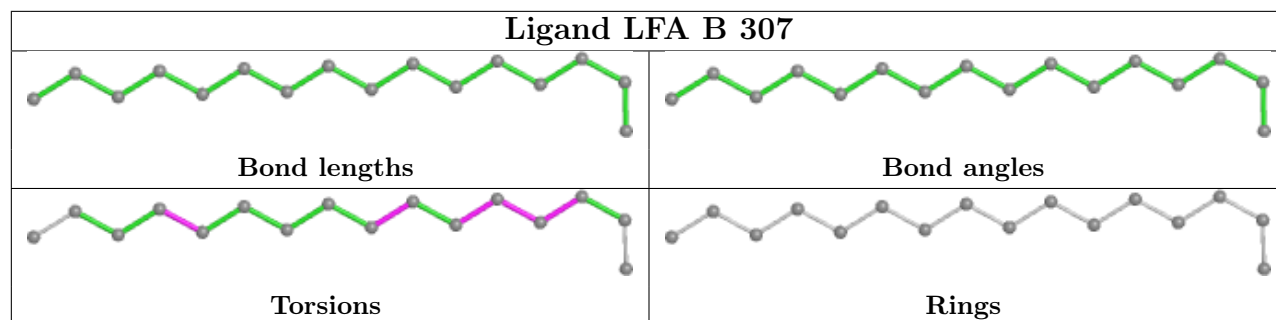


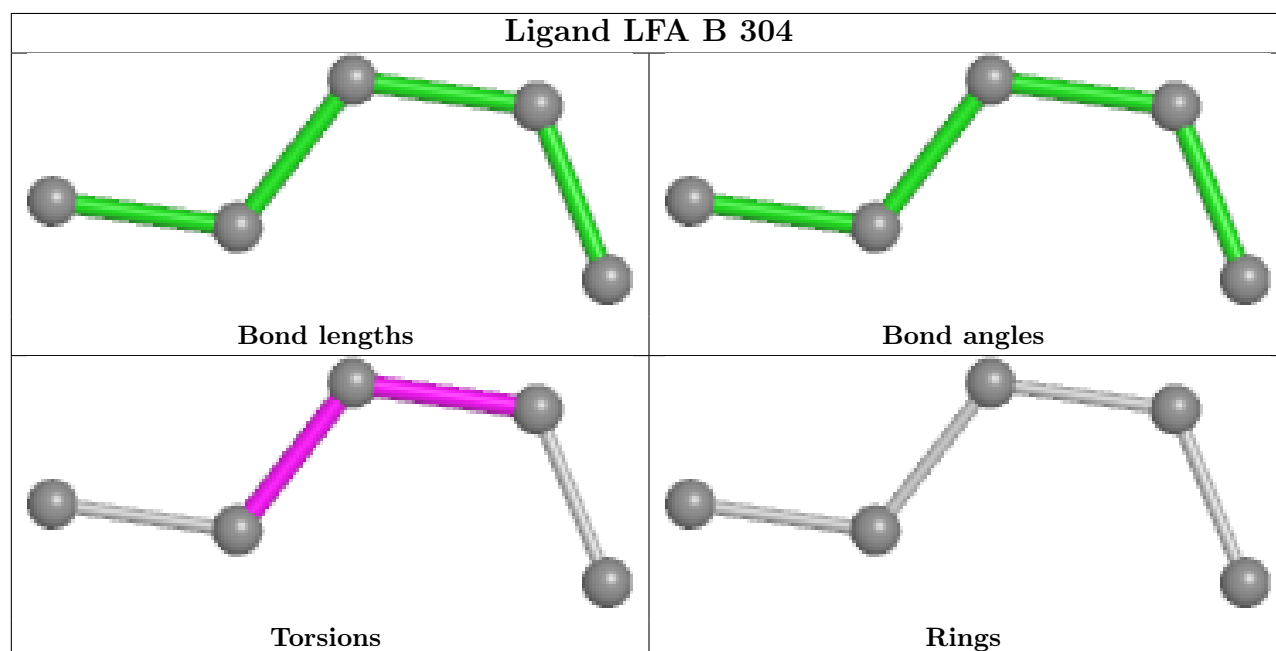
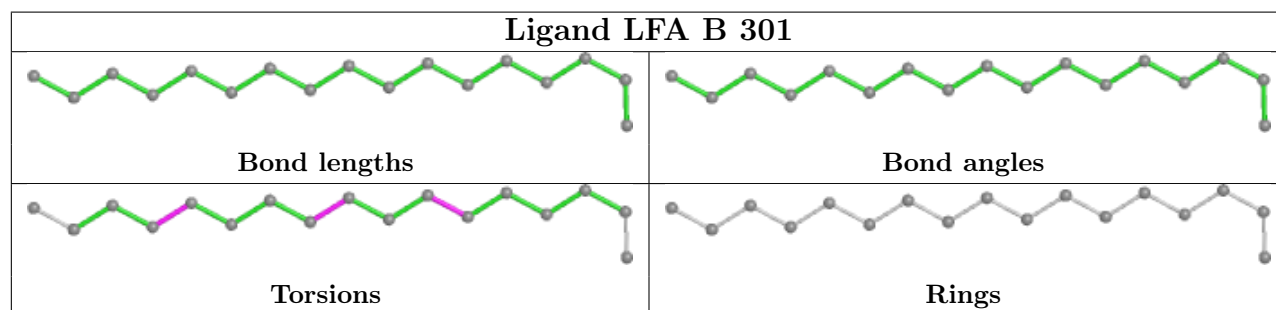
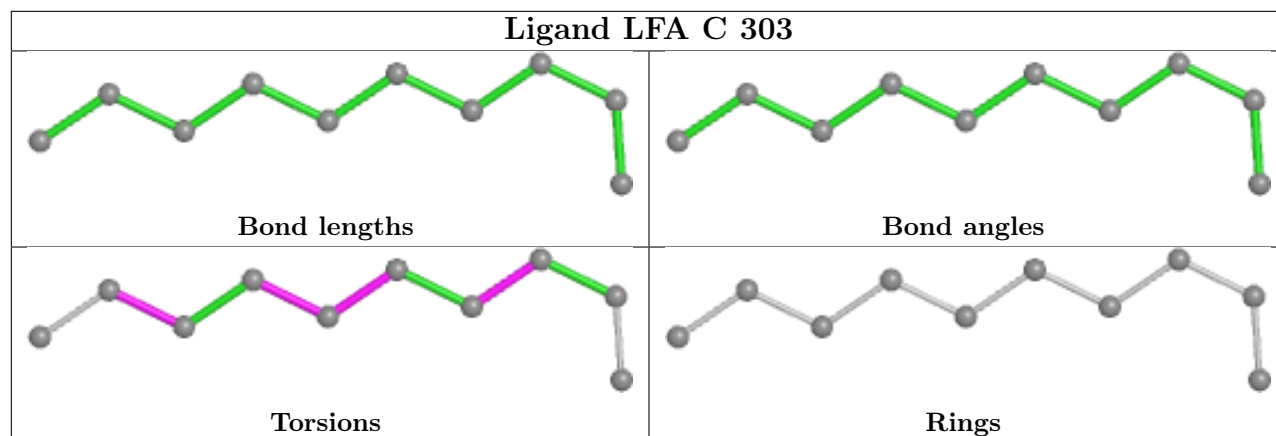


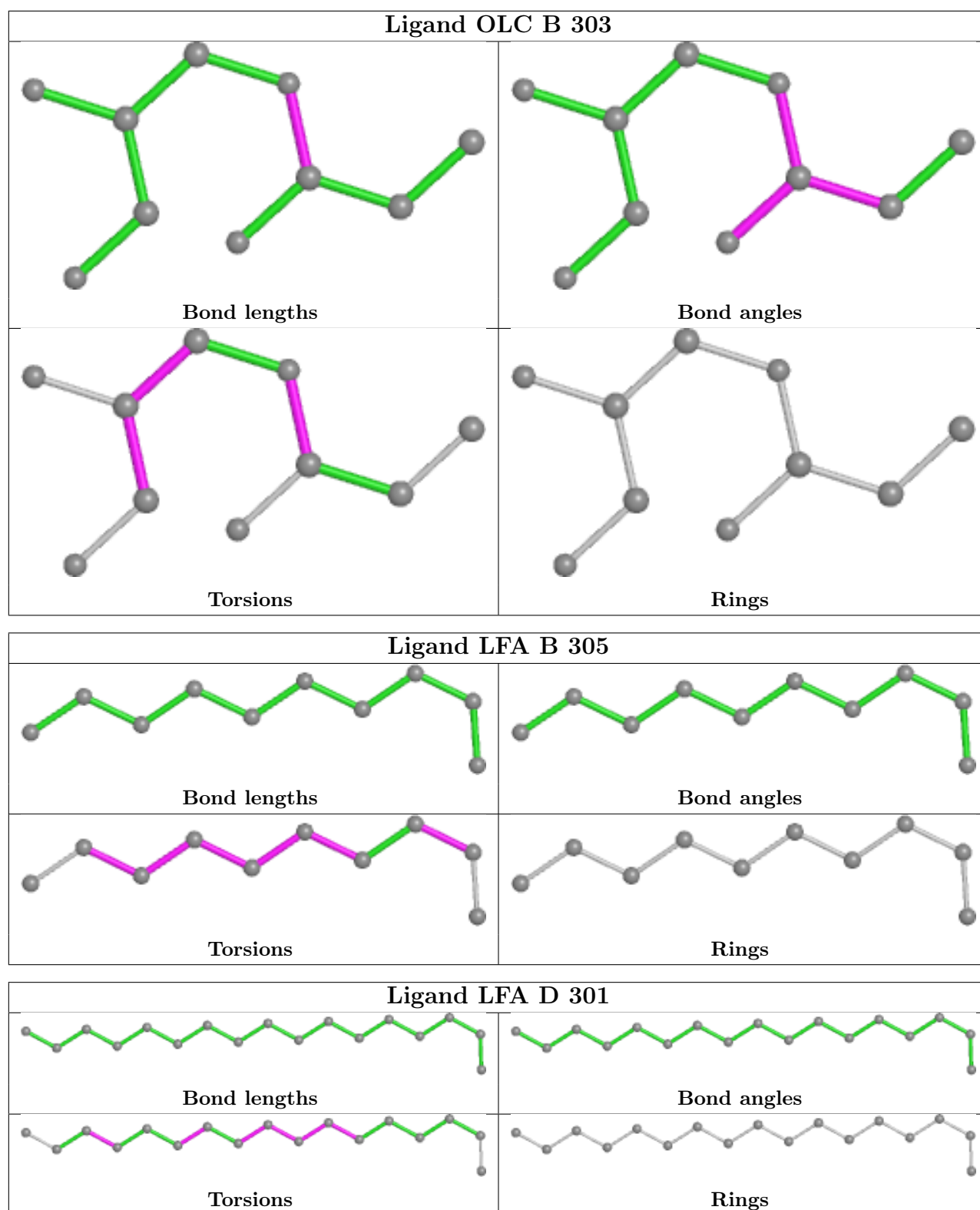


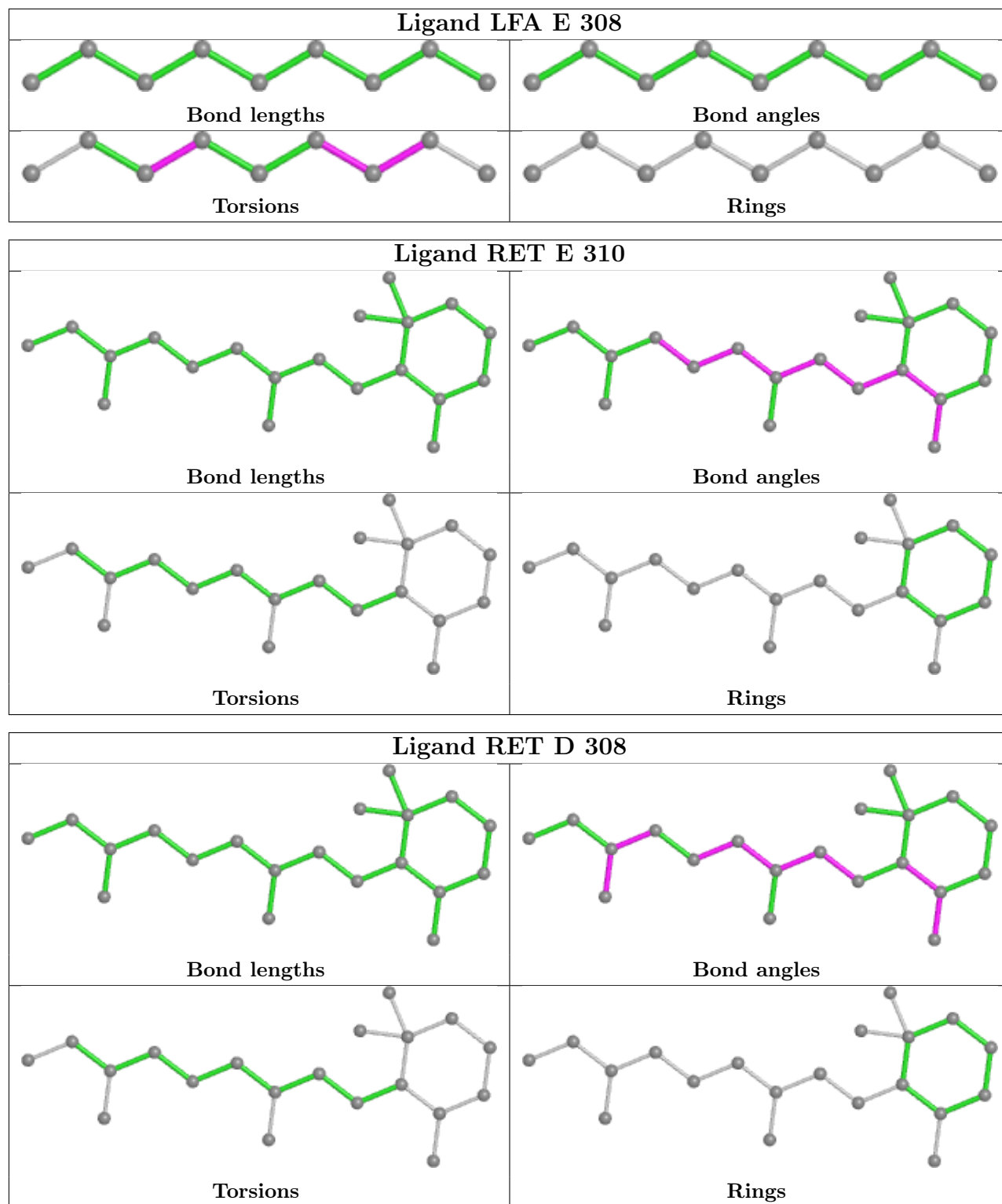


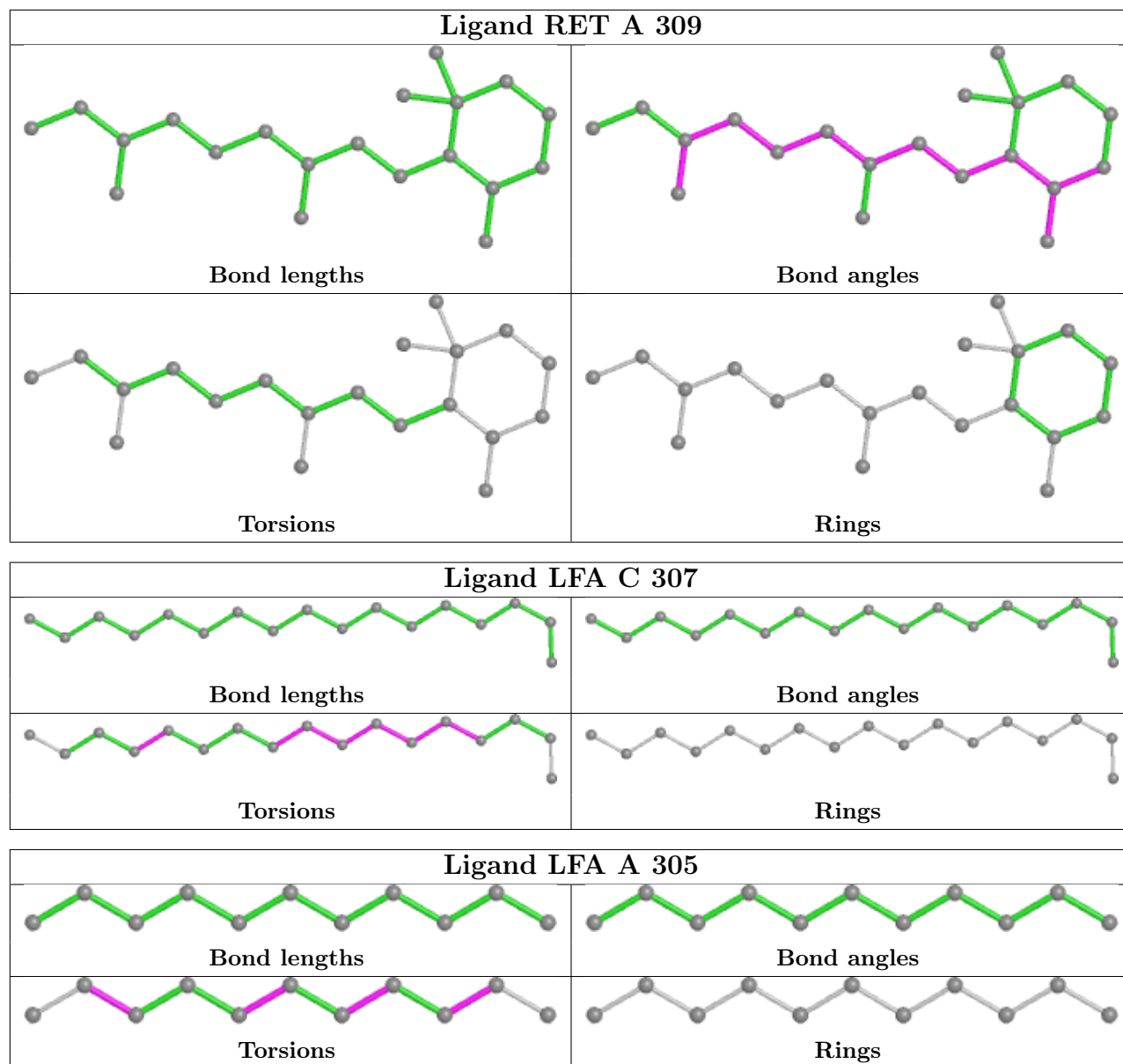


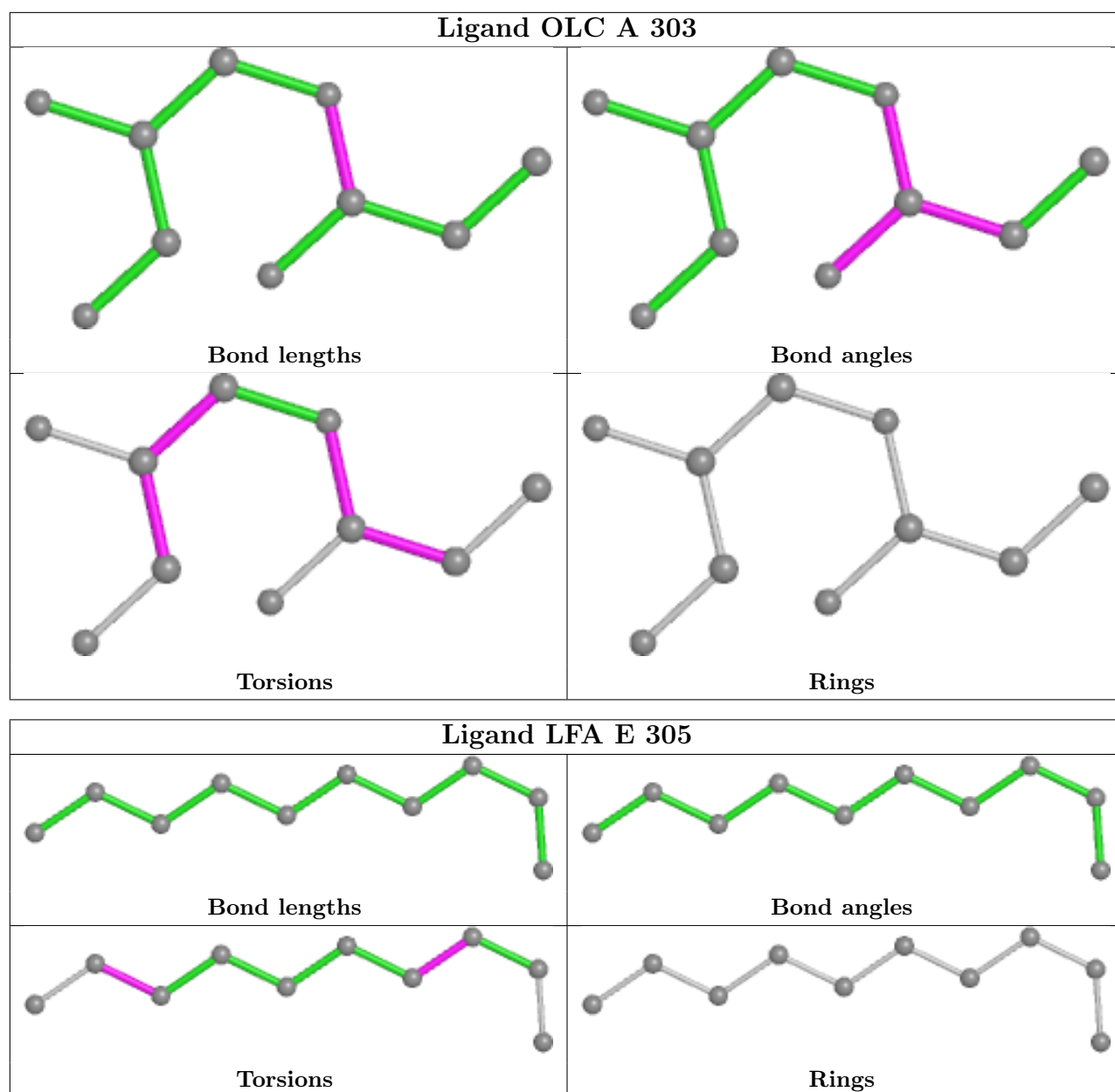












## 5.7 Other polymers [i](#)

There are no such residues in this entry.

## 5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 6 Fit of model and data [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	273/273 (100%)	0.10	18 (6%) 18 13	56, 71, 100, 154	0
1	B	273/273 (100%)	0.18	16 (5%) 22 17	56, 73, 100, 165	0
1	C	273/273 (100%)	0.17	15 (5%) 25 19	53, 71, 98, 168	0
1	D	270/273 (98%)	0.24	15 (5%) 24 19	54, 74, 100, 143	0
1	E	273/273 (100%)	0.12	14 (5%) 28 22	58, 73, 100, 160	0
All	All	1362/1365 (99%)	0.16	78 (5%) 23 18	53, 72, 100, 168	0

The worst 5 of 78 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	274	GLU	5.9
1	D	69	VAL	5.4
1	B	274	GLU	4.6
1	B	230	VAL	4.4
1	A	275	LEU	4.2

### 6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

### 6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

### 6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum,



median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

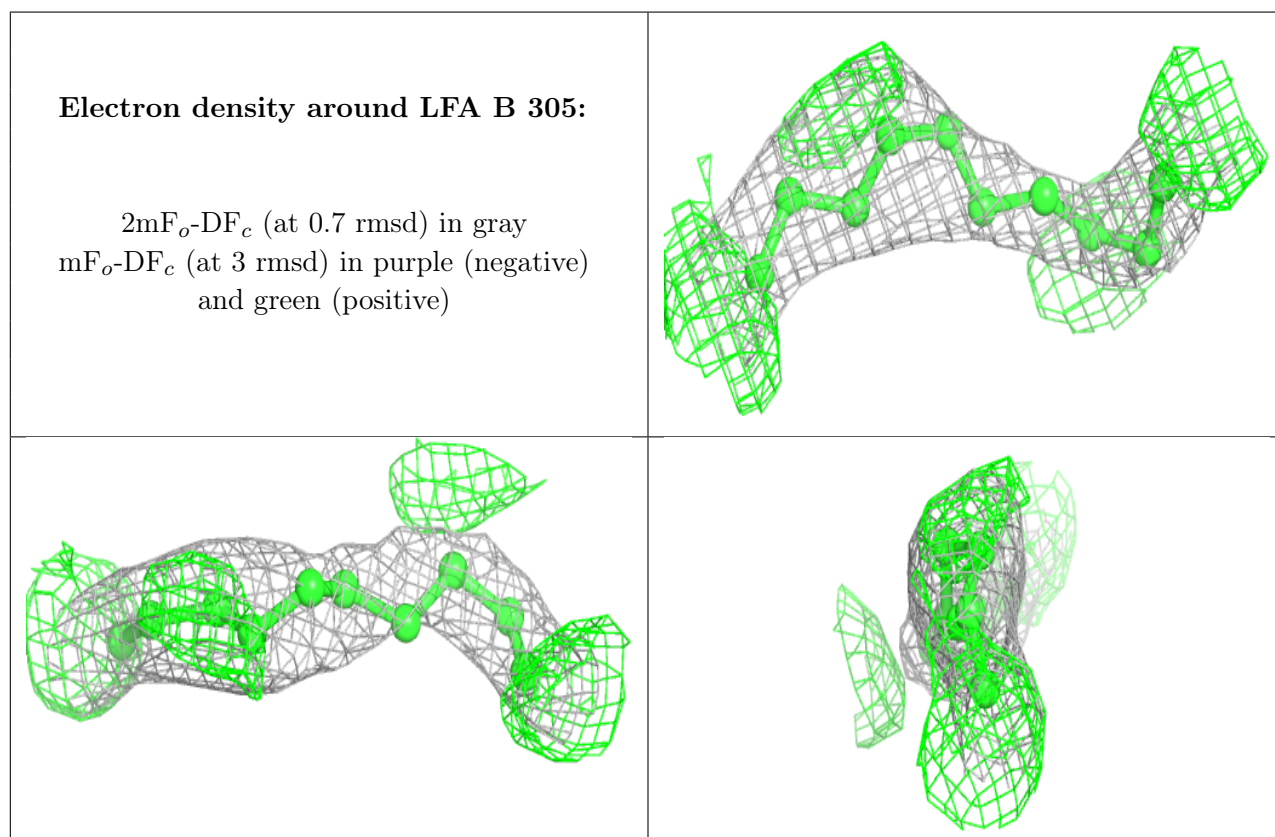
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
2	LFA	B	305	10/20	0.71	0.20	91,109,131,133	0
2	LFA	B	304	5/20	0.73	0.34	91,91,98,101	0
2	LFA	C	307	17/20	0.76	0.85	80,94,111,117	0
2	LFA	C	308	7/20	0.76	0.32	80,88,95,99	0
4	NA	E	309	1/1	0.76	0.10	70,70,70,70	0
2	LFA	E	307	9/20	0.79	0.14	93,104,117,119	0
2	LFA	A	302	16/20	0.80	0.90	76,87,99,106	0
3	OLC	B	303	10/25	0.80	0.43	77,100,111,125	0
2	LFA	E	305	10/20	0.80	0.19	85,102,108,111	0
2	LFA	E	306	15/20	0.81	0.30	84,94,110,111	0
2	LFA	A	307	7/20	0.81	0.32	83,91,112,114	0
2	LFA	D	303	5/20	0.81	0.20	87,88,97,98	0
4	NA	C	309	1/1	0.81	0.11	69,69,69,69	0
2	LFA	A	306	15/20	0.81	0.33	82,102,111,112	0
2	LFA	C	304	5/20	0.82	0.20	76,83,93,93	0
2	LFA	C	306	10/20	0.83	0.15	81,94,107,107	0
2	LFA	C	303	10/20	0.83	0.16	90,93,106,109	0
2	LFA	B	307	16/20	0.84	0.85	68,86,102,103	0
2	LFA	D	304	16/20	0.85	0.32	86,105,110,113	0
3	OLC	D	302	9/25	0.85	0.29	70,97,109,112	0
2	LFA	D	305	6/20	0.85	0.22	95,100,102,104	0
2	LFA	D	306	16/20	0.85	1.07	80,90,101,101	0
3	OLC	C	302	11/25	0.86	0.29	68,98,118,128	0
2	LFA	E	302	16/20	0.86	0.89	80,90,97,97	0
2	LFA	E	304	5/20	0.86	0.18	81,82,95,99	0
2	LFA	A	305	11/20	0.86	0.12	91,99,124,127	0
2	LFA	B	302	18/20	0.87	0.26	91,105,116,117	0
3	OLC	A	303	10/25	0.88	0.30	77,99,105,114	0
3	OLC	E	303	10/25	0.88	0.24	68,90,98,101	0
2	LFA	C	301	19/20	0.88	0.32	69,81,97,103	0
4	NA	D	307	1/1	0.88	0.11	71,71,71,71	0
2	LFA	E	308	9/20	0.88	0.24	87,95,106,112	0
2	LFA	E	301	15/20	0.89	0.39	73,80,87,90	0
2	LFA	C	305	16/20	0.89	0.25	79,98,107,109	0
2	LFA	B	306	6/20	0.89	0.21	74,86,92,94	0
2	LFA	A	304	5/20	0.91	0.22	74,86,88,90	0
2	LFA	D	301	17/20	0.91	0.38	73,82,90,98	0
4	NA	A	308	1/1	0.91	0.10	71,71,71,71	0
2	LFA	A	301	18/20	0.92	0.27	68,77,86,89	0
2	LFA	B	301	17/20	0.95	0.31	58,70,89,95	0
5	RET	A	309	20/21	0.95	0.17	60,69,76,81	0

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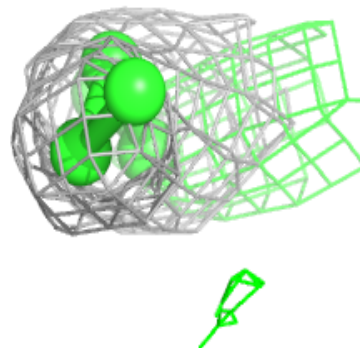
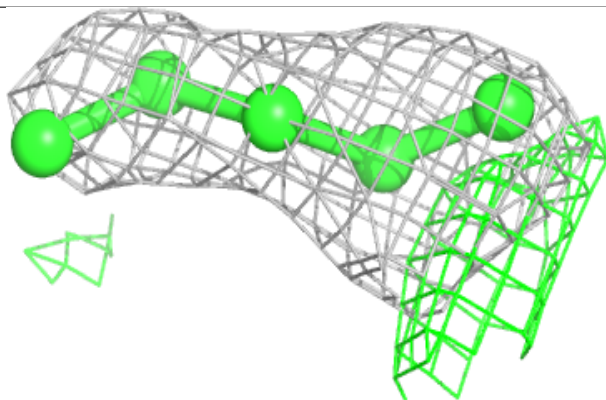
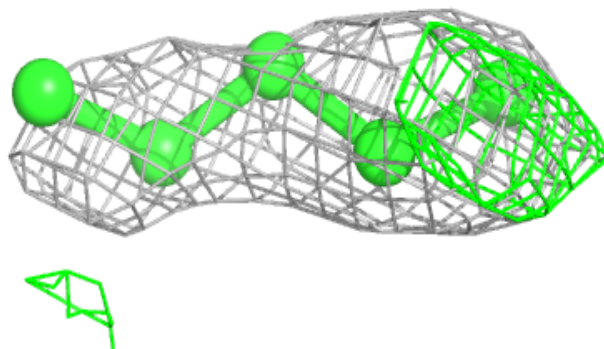
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
5	RET	B	309	20/21	0.95	0.17	55,67,75,92	0
4	NA	B	308	1/1	0.96	0.12	67,67,67,67	0
5	RET	D	308	20/21	0.96	0.20	61,74,83,89	0
5	RET	C	310	20/21	0.97	0.18	58,68,78,89	0
5	RET	E	310	20/21	0.97	0.15	64,71,79,79	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

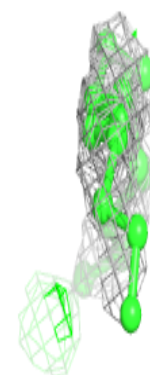
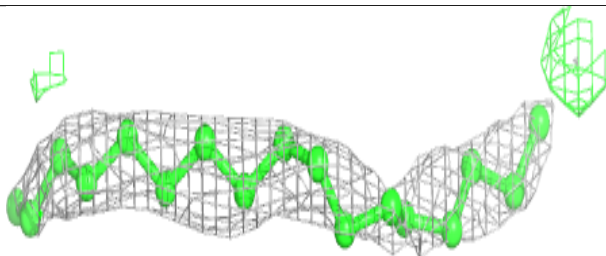
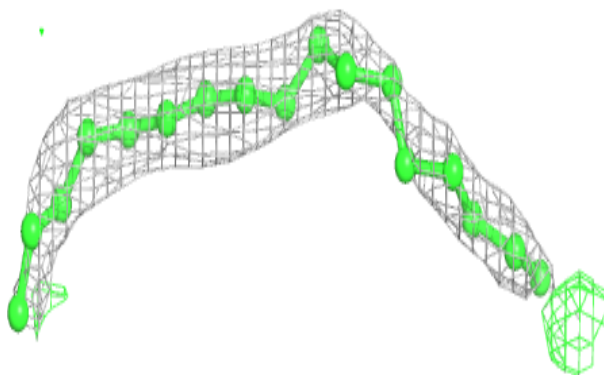


**Electron density around LFA B 304:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

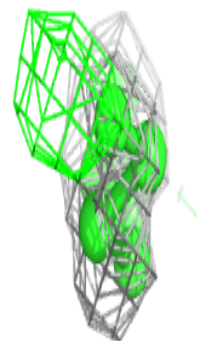
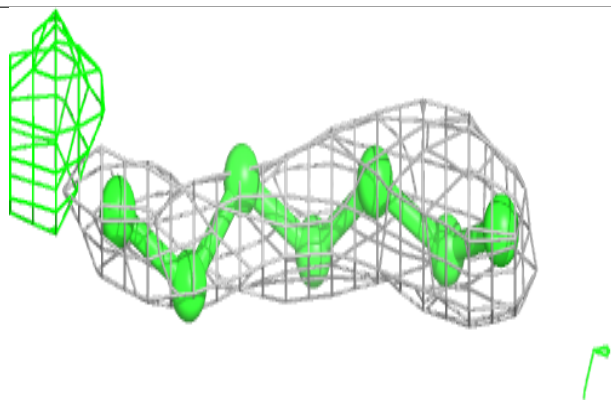
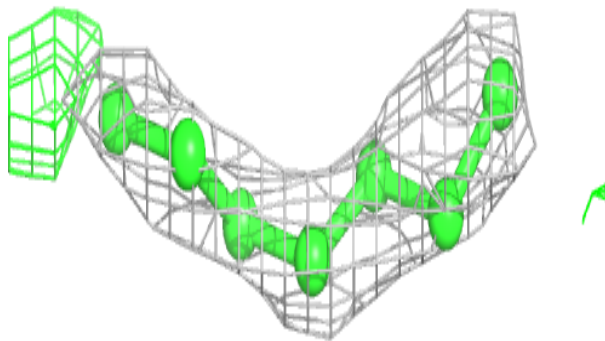
**Electron density around LFA C 307:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

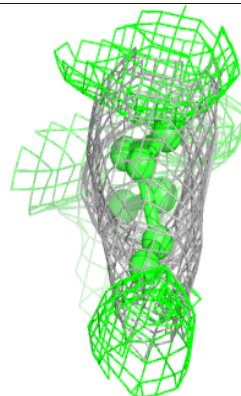
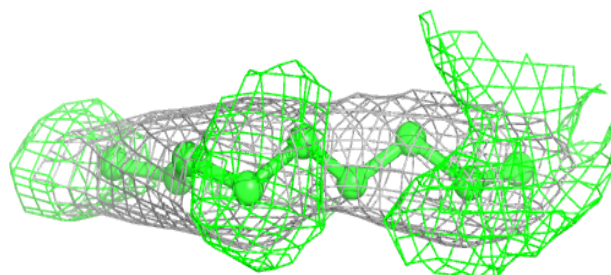
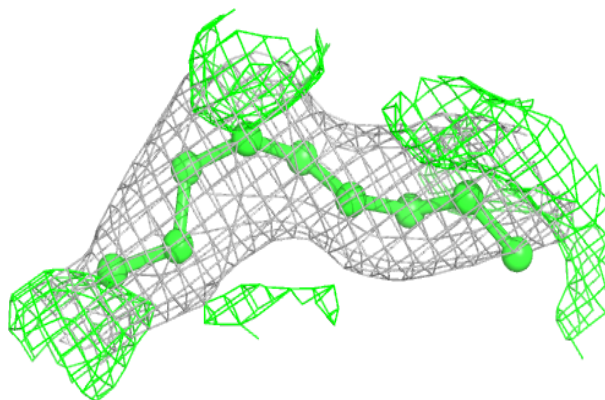


**Electron density around LFA C 308:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around LFA E 307:**

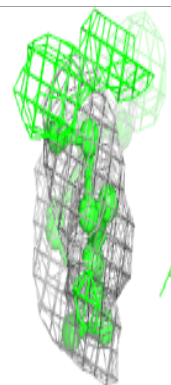
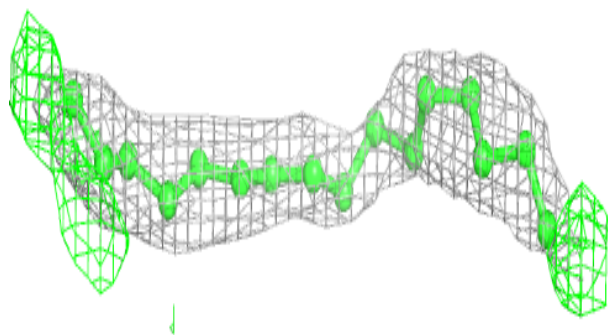
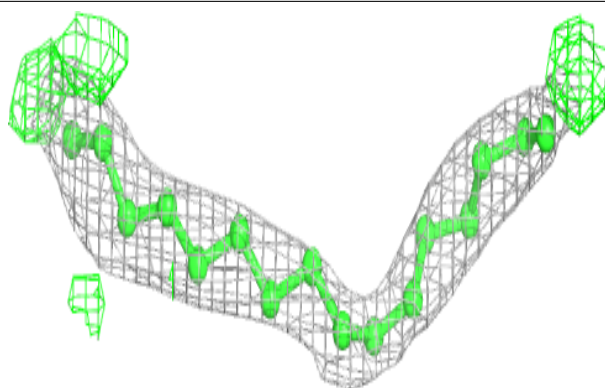
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



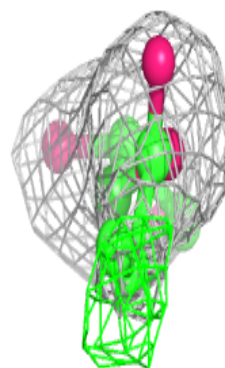
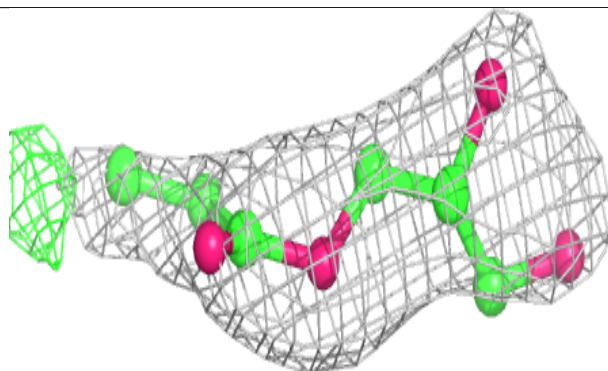
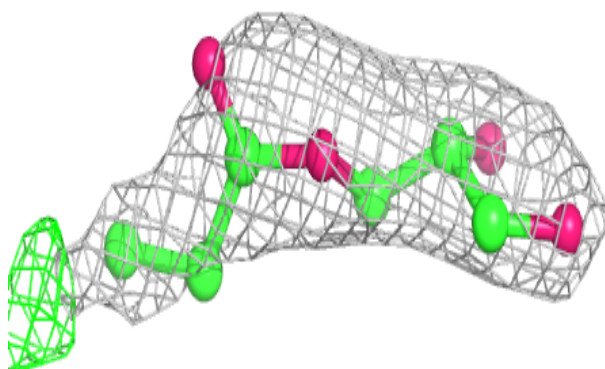


**Electron density around LFA A 302:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

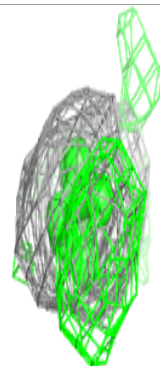
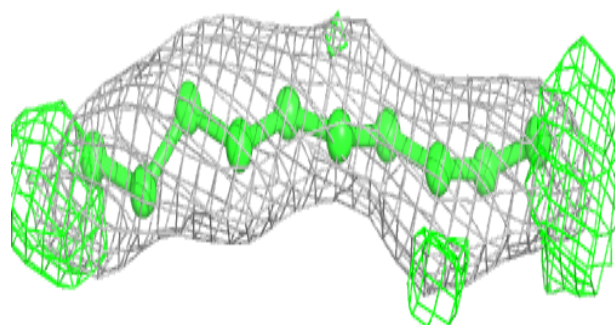
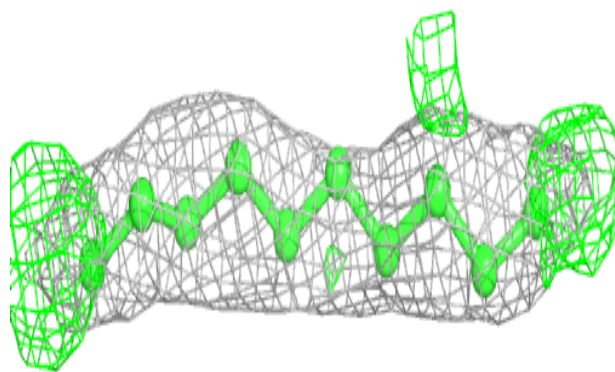
**Electron density around OLC B 303:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

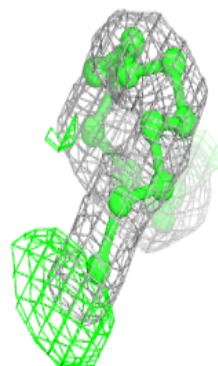
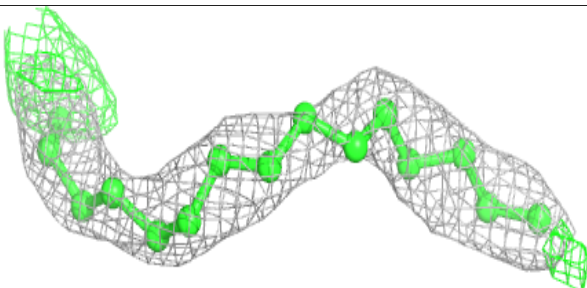
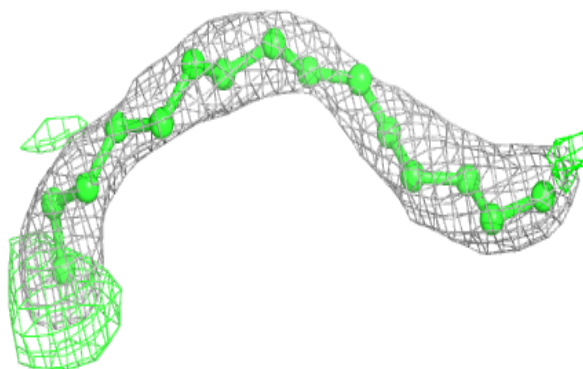


**Electron density around LFA E 305:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

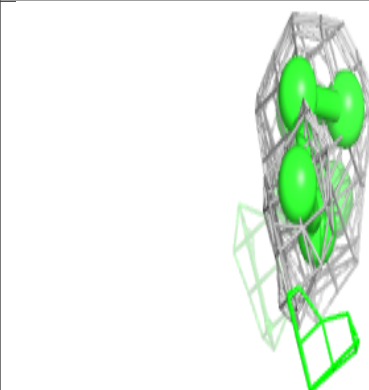
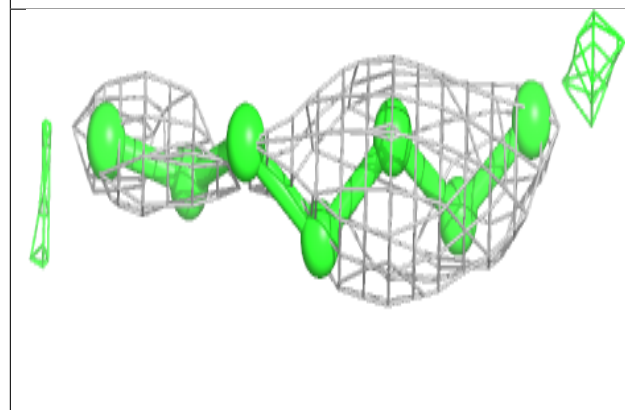
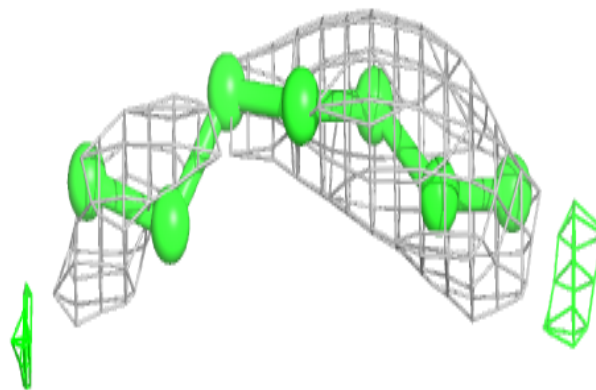
**Electron density around LFA E 306:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

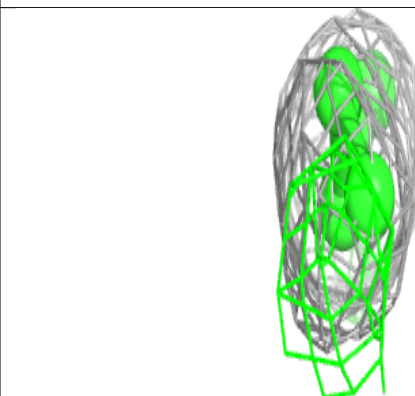
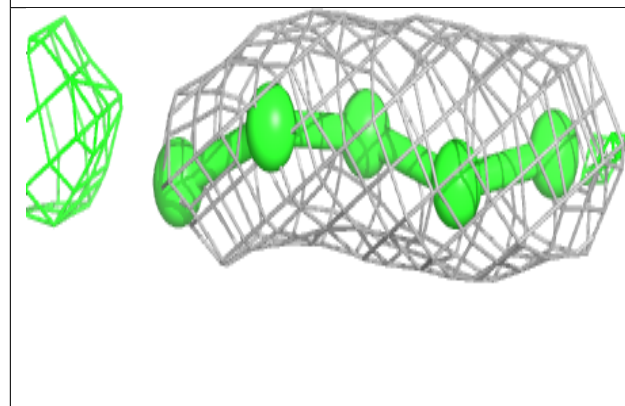
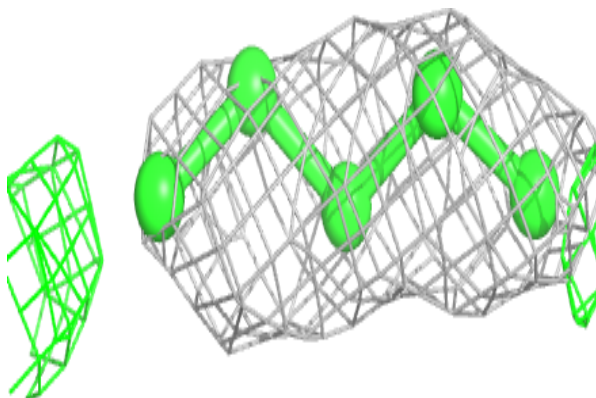


**Electron density around LFA A 307:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

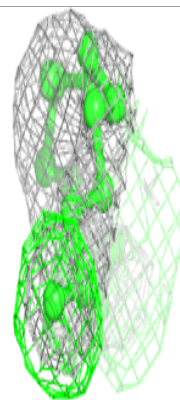
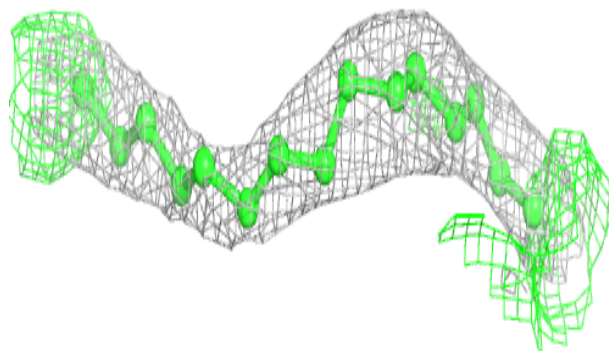
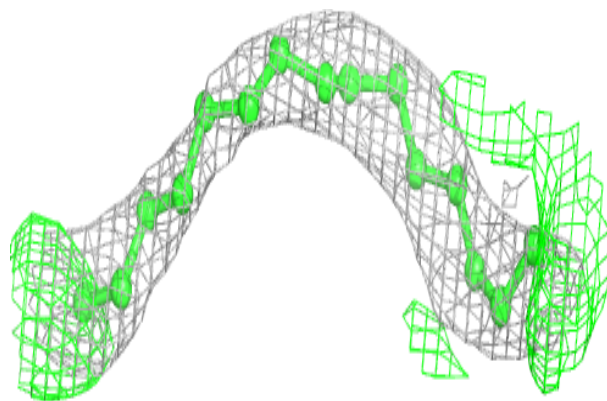
**Electron density around LFA D 303:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

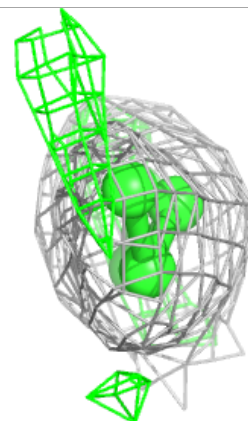
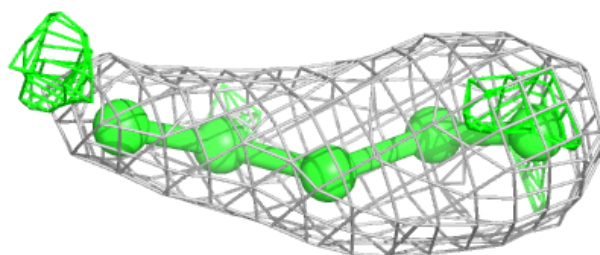
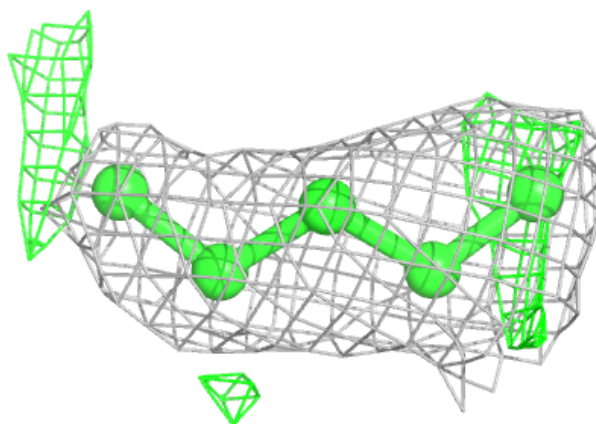


**Electron density around LFA A 306:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around LFA C 304:**

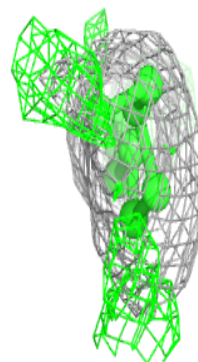
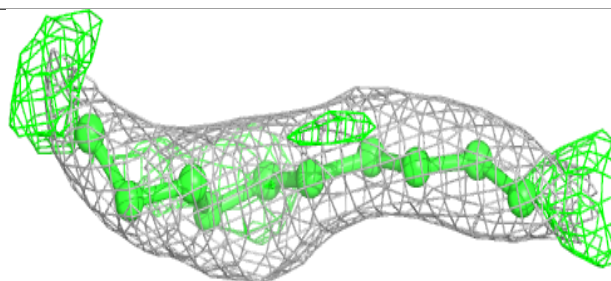
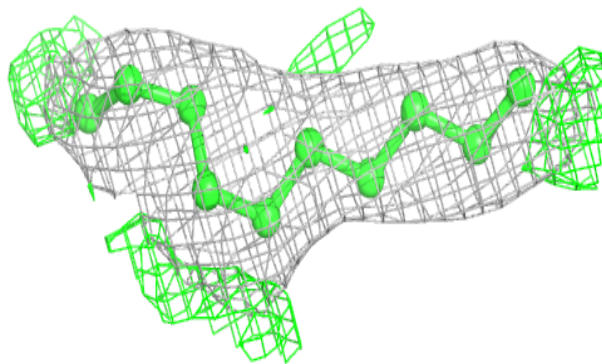
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



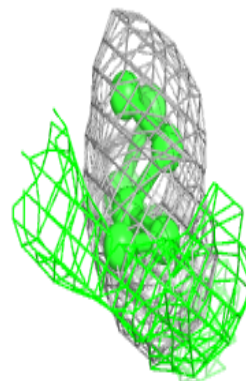
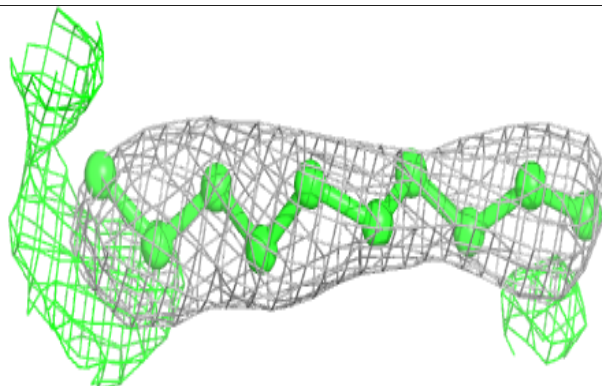
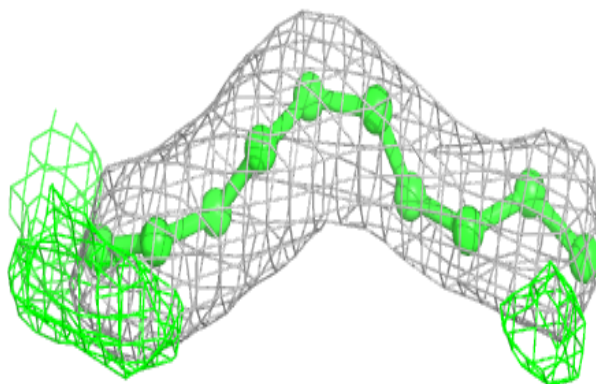


**Electron density around LFA C 306:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

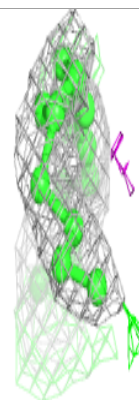
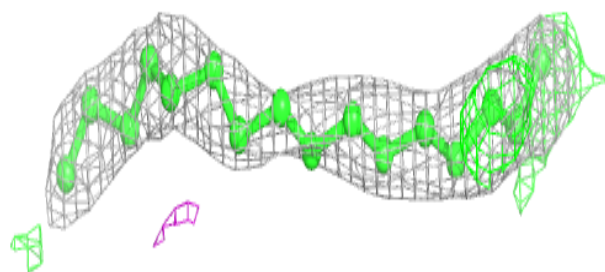
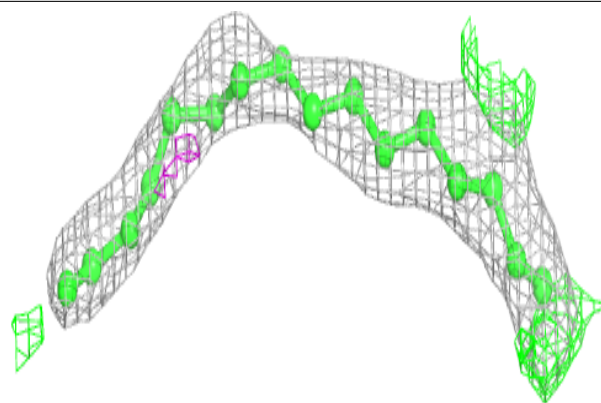
**Electron density around LFA C 303:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

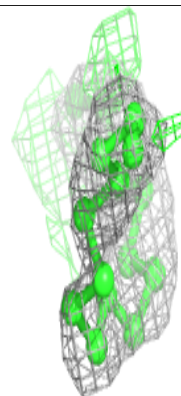
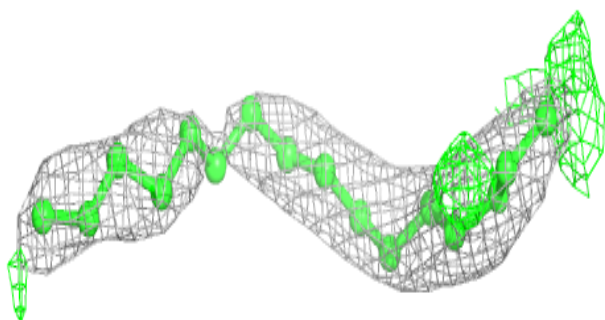
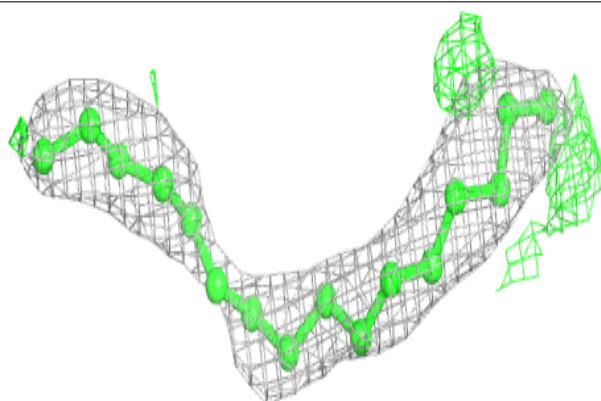


**Electron density around LFA B 307:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

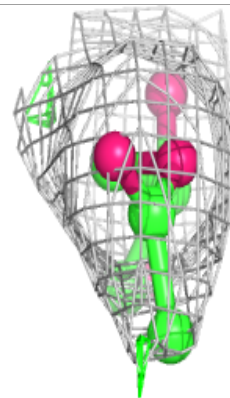
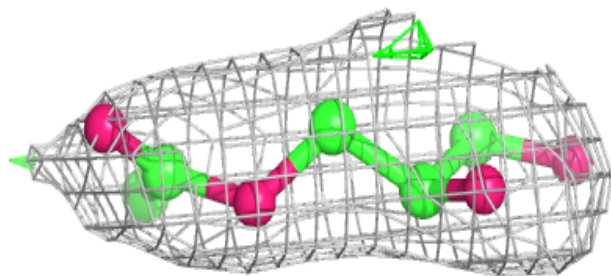
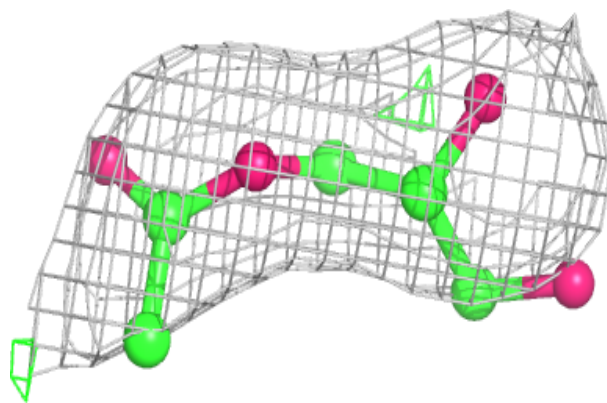
**Electron density around LFA D 304:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

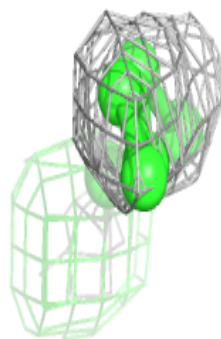
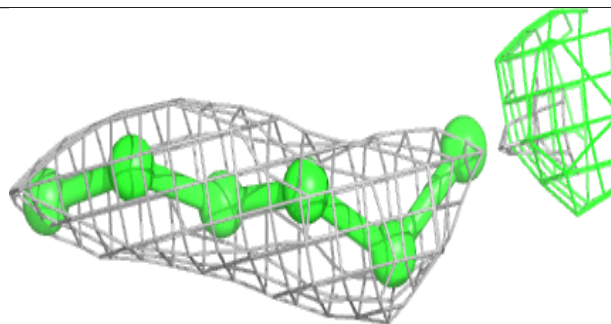
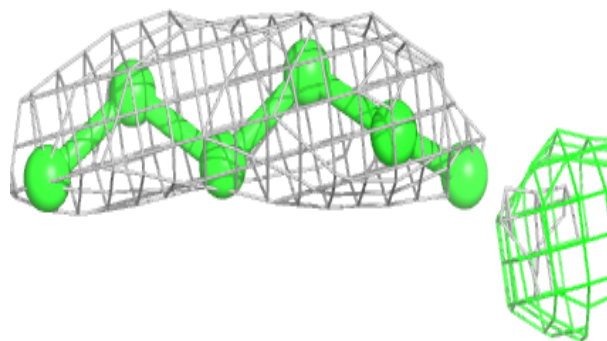


**Electron density around OLC D 302:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

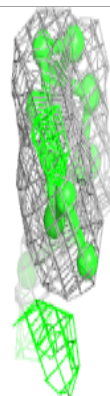
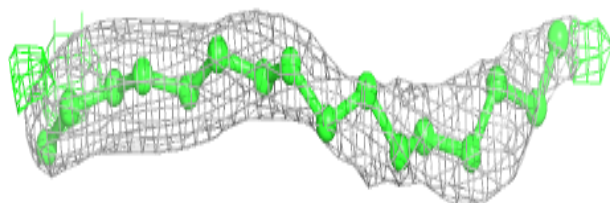
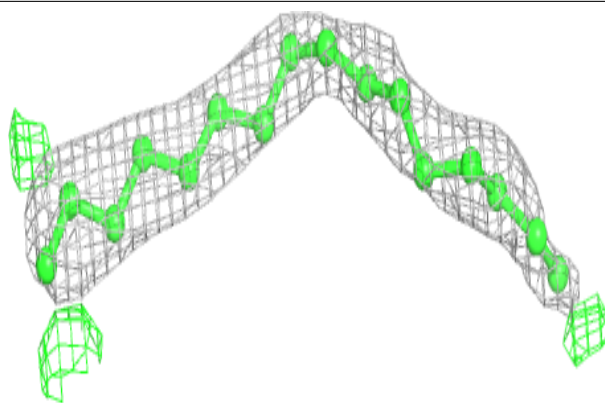
**Electron density around LFA D 305:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

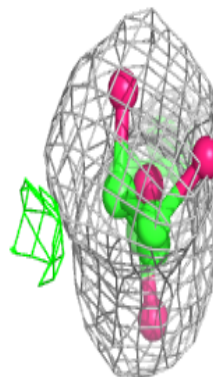
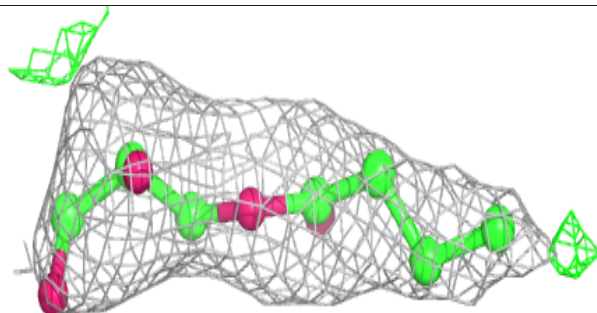
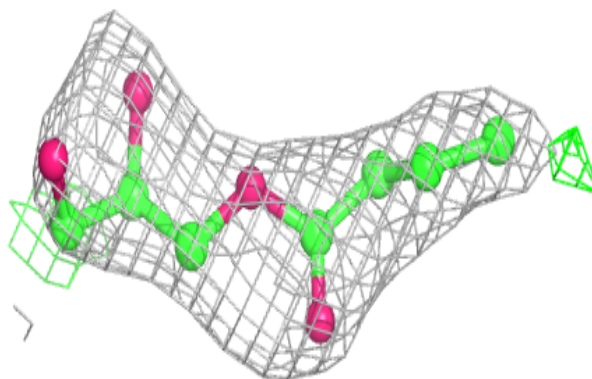


**Electron density around LFA D 306:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around OLC C 302:**

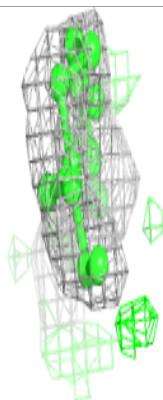
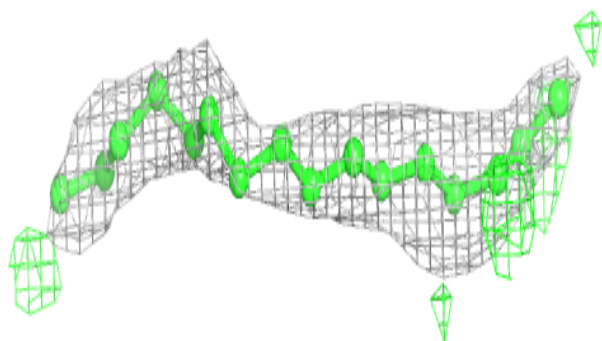
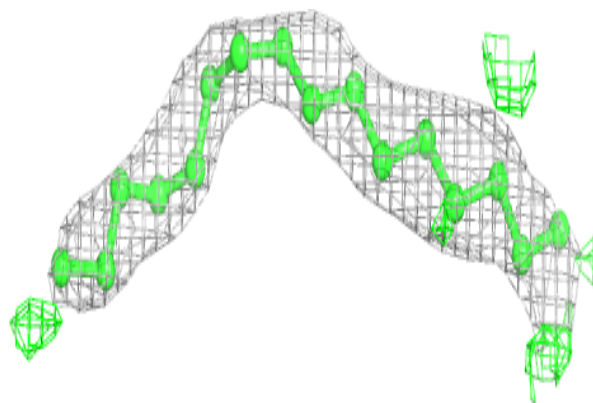
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



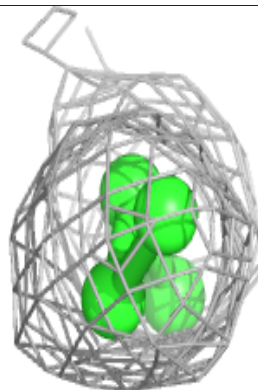
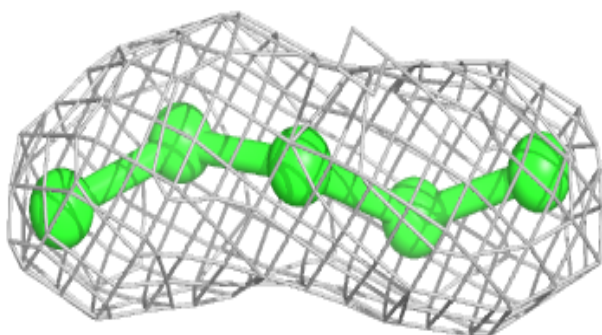
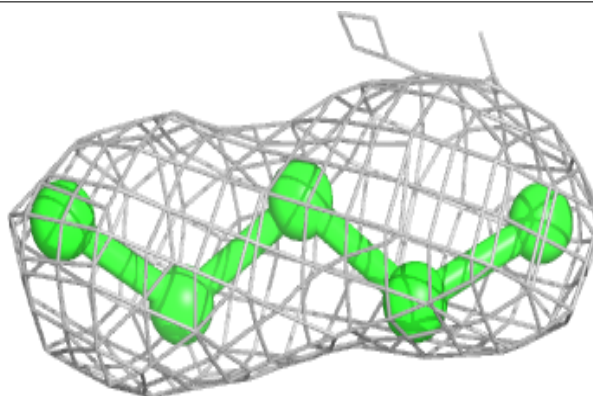


**Electron density around LFA E 302:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

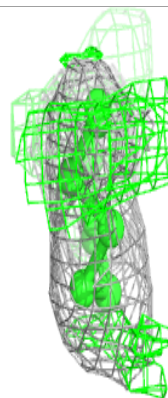
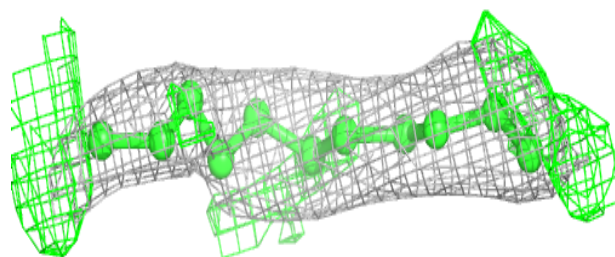
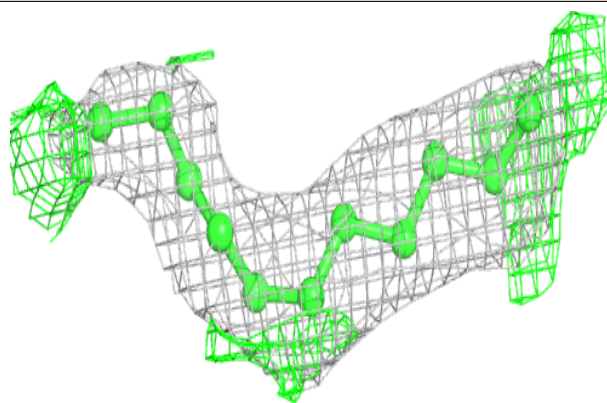
**Electron density around LFA E 304:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

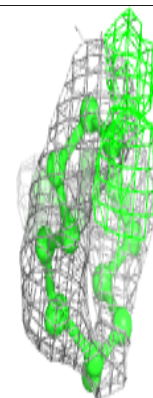
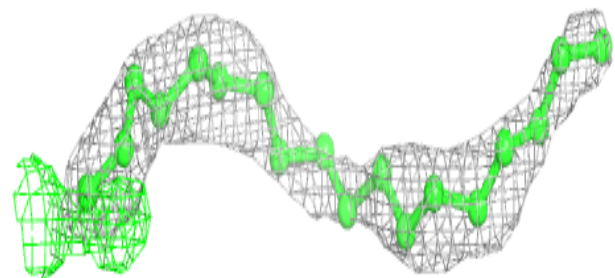
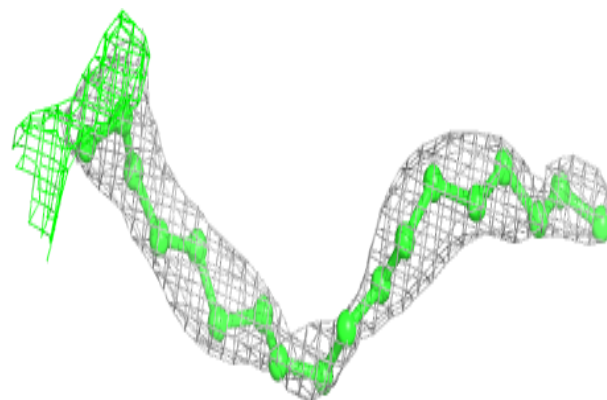


**Electron density around LFA A 305:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

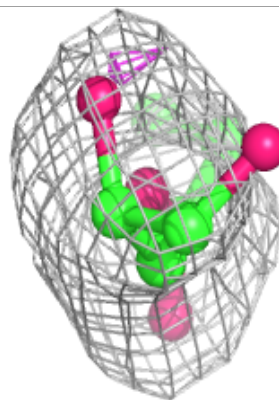
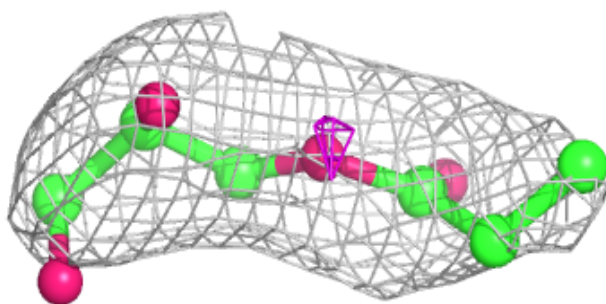
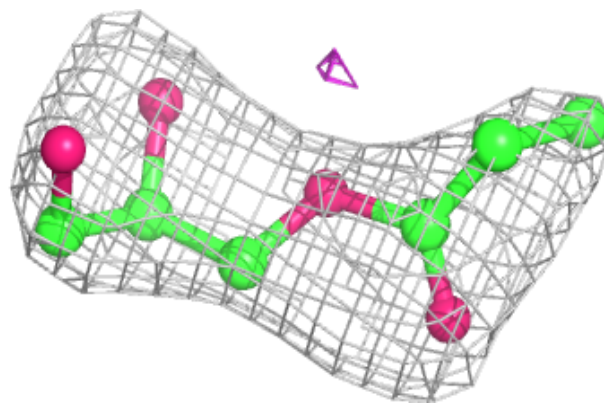
**Electron density around LFA B 302:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

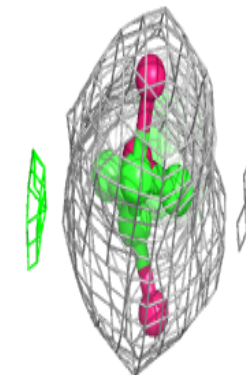
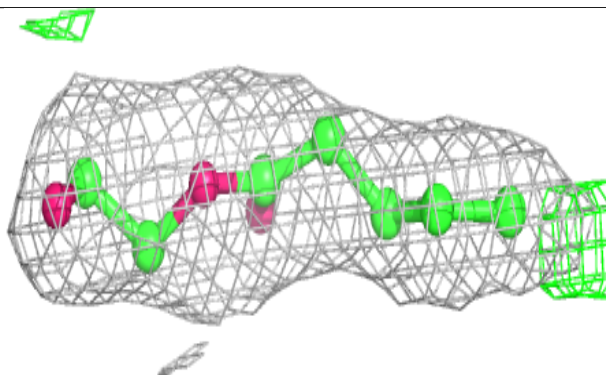
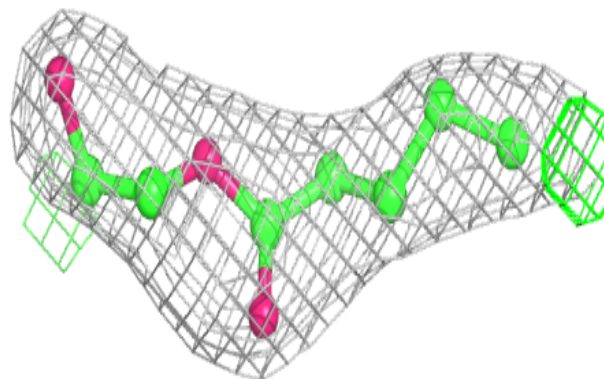


**Electron density around OLC A 303:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

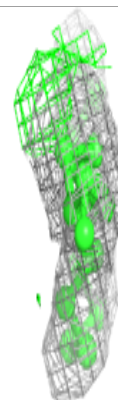
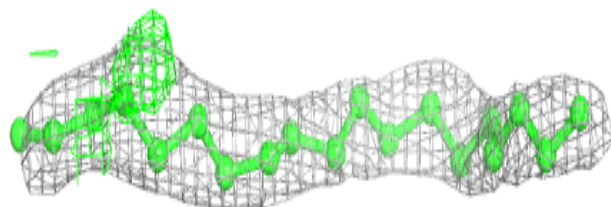
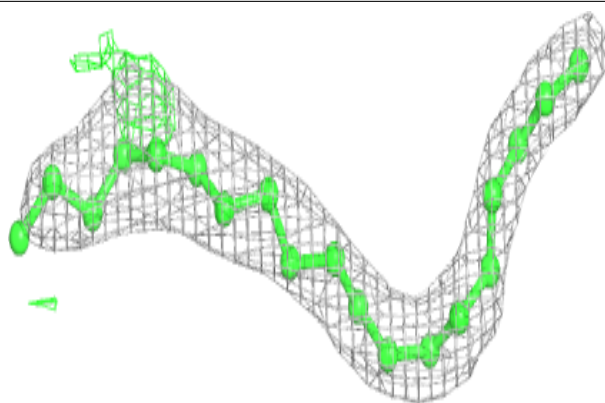
**Electron density around OLC E 303:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

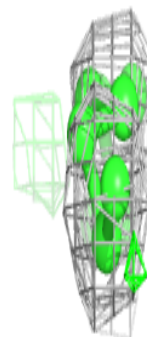
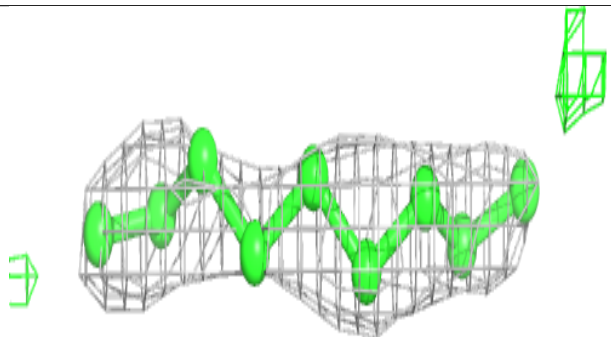
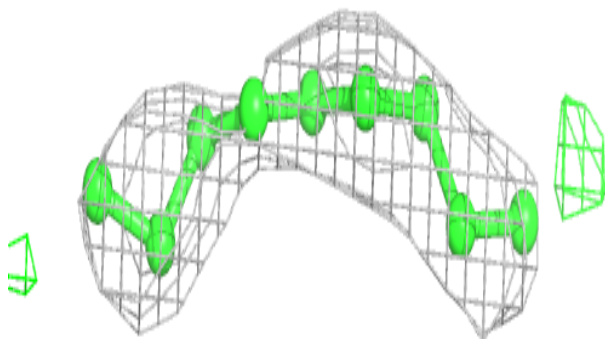


**Electron density around LFA C 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around LFA E 308:**

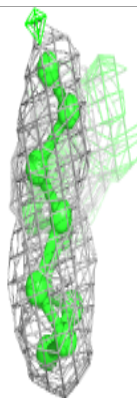
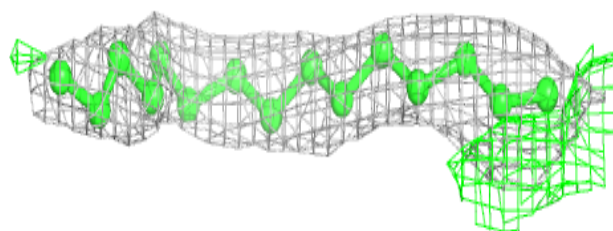
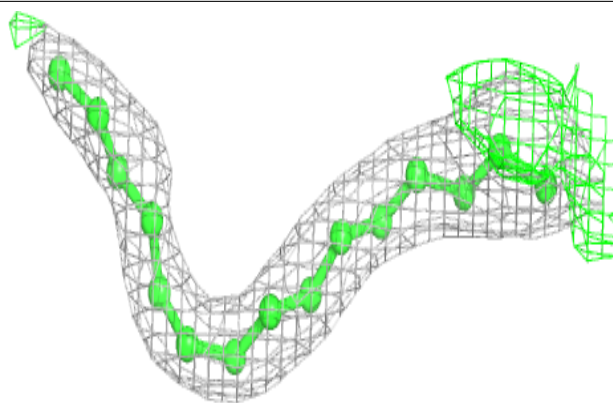
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



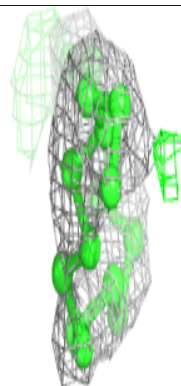
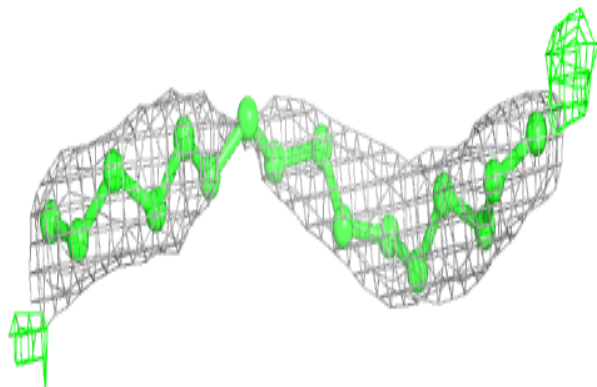
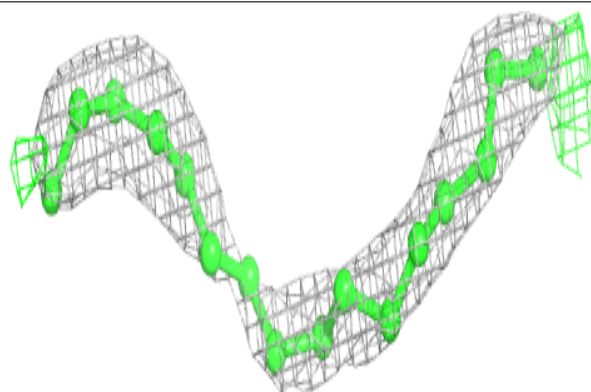


**Electron density around LFA E 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

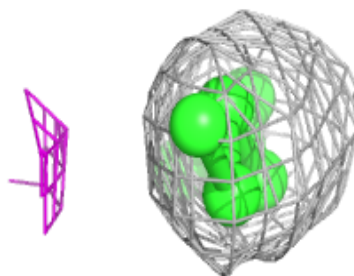
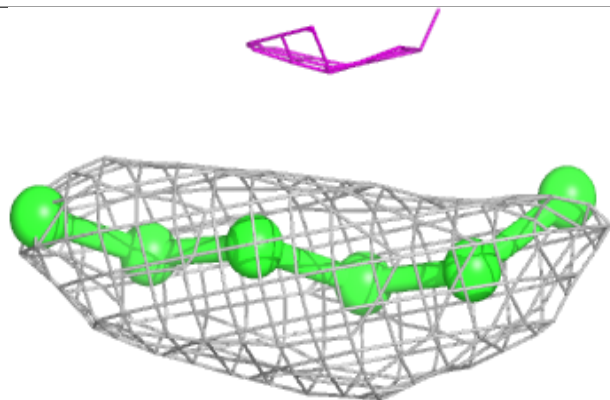
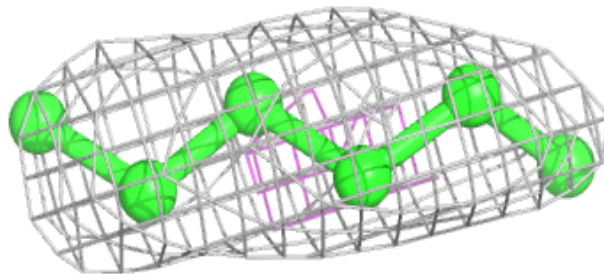
**Electron density around LFA C 305:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

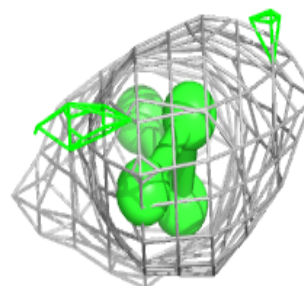
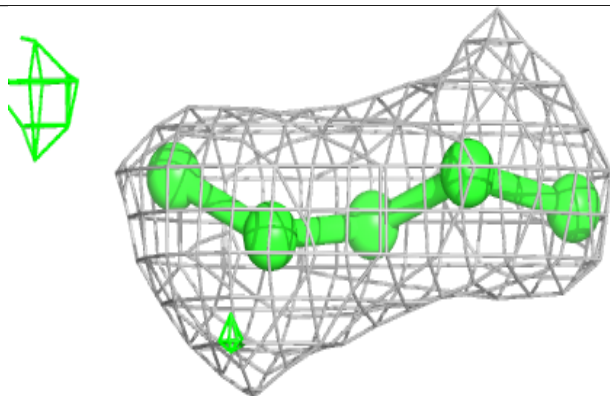
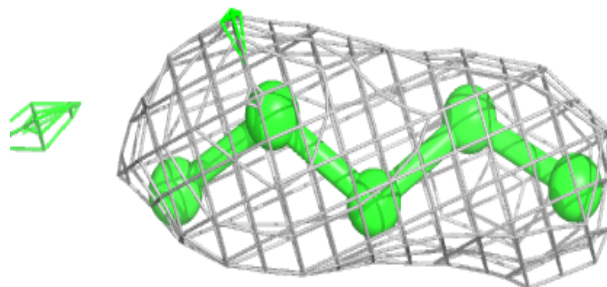


**Electron density around LFA B 306:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

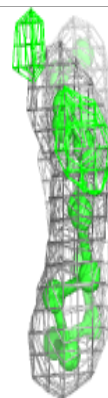
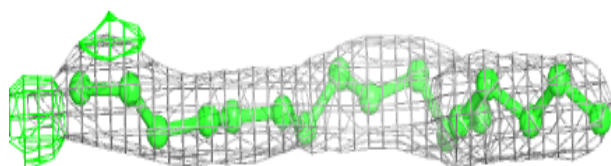
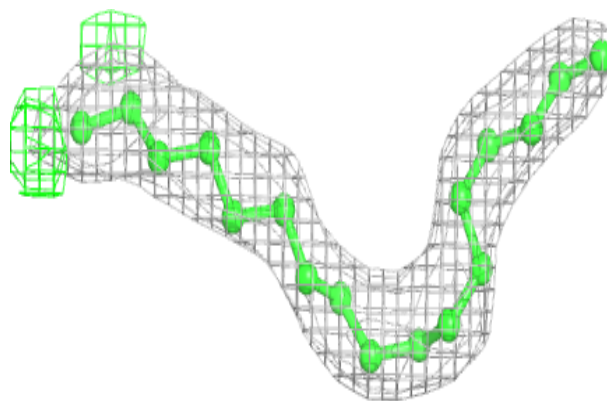
**Electron density around LFA A 304:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

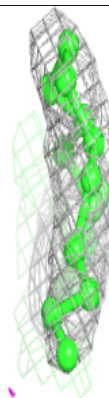
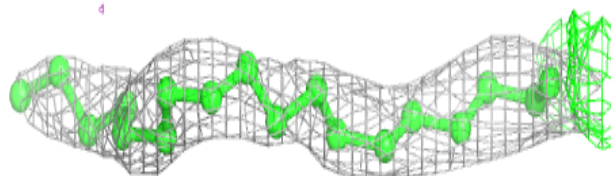
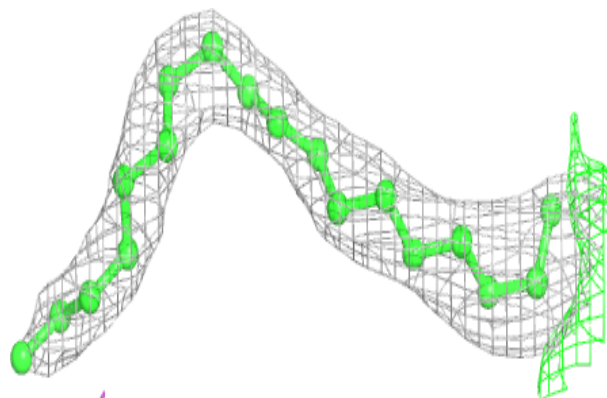


**Electron density around LFA D 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

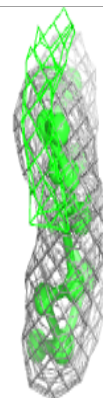
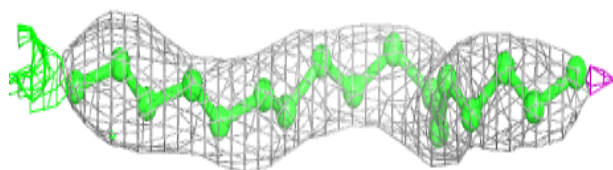
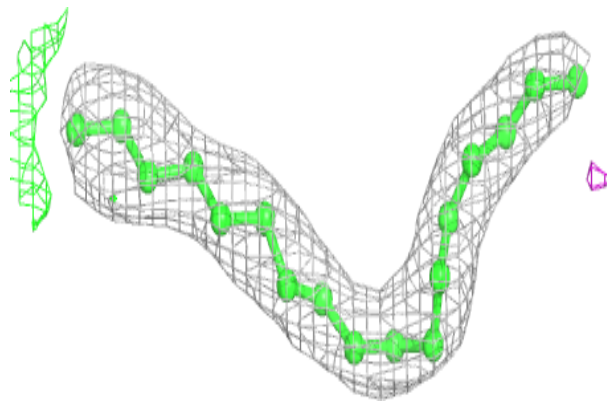
**Electron density around LFA A 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

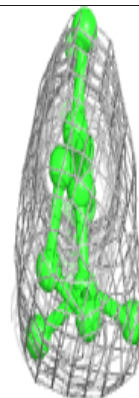
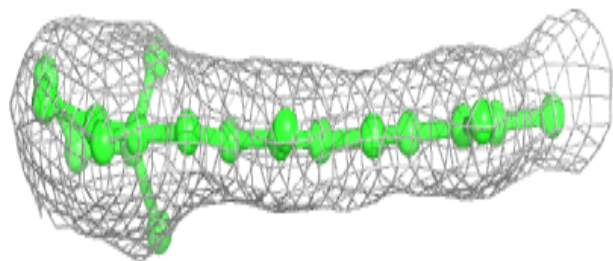
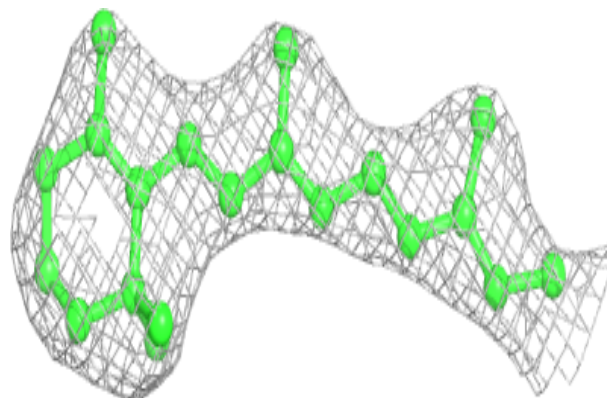


**Electron density around LFA B 301:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around RET A 309:**

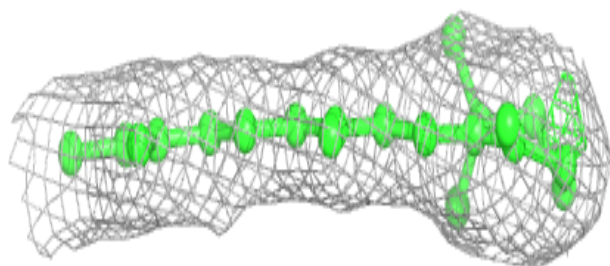
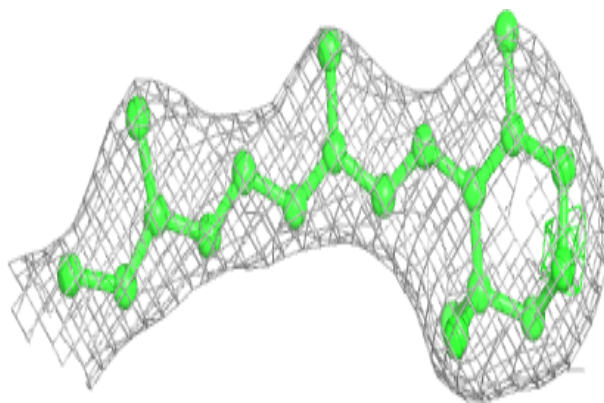
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



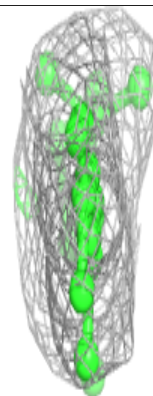
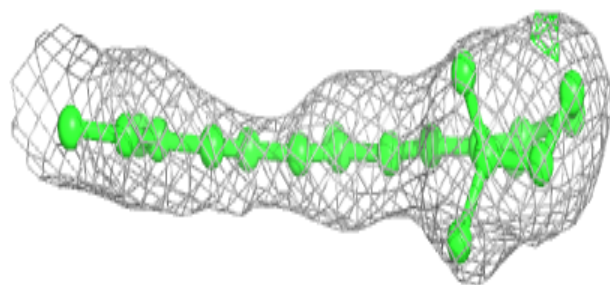
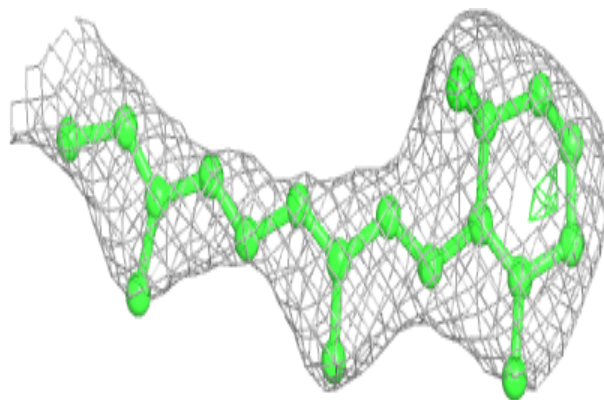


**Electron density around RET B 309:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

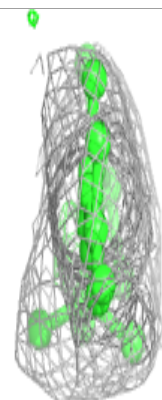
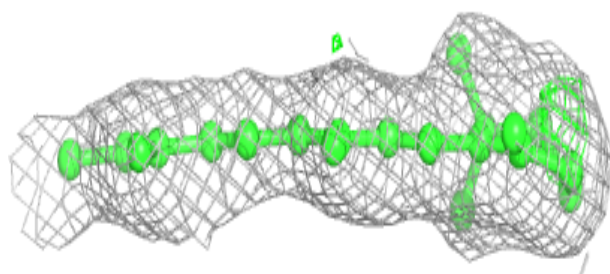
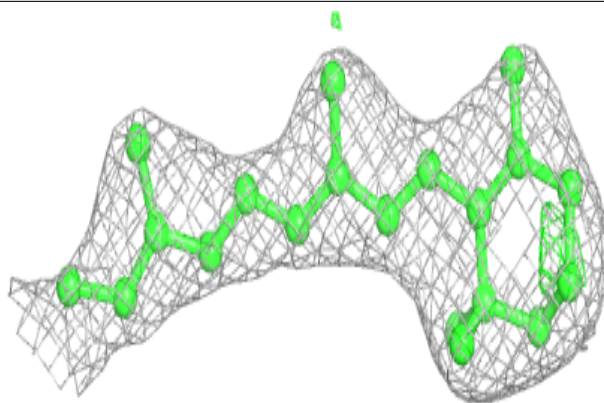
**Electron density around RET D 308:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

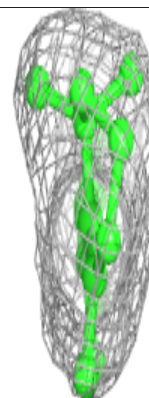
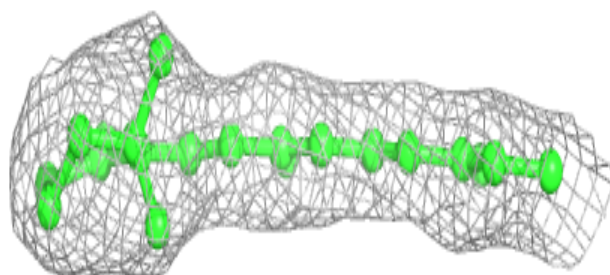
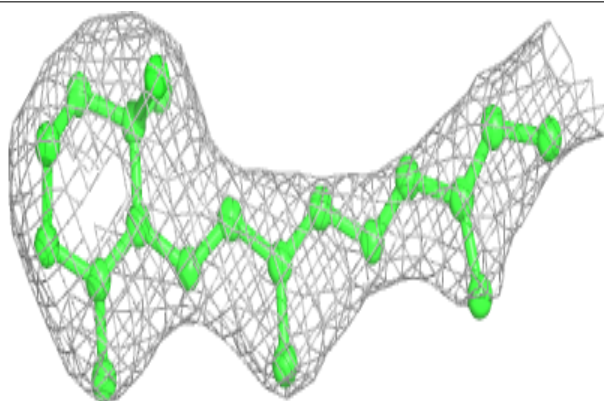


**Electron density around RET C 310:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

**Electron density around RET E 310:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.